GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2005, 15:38:47 ; Search time 8644.89 Seconds
(without alignments)
12117.322 Million cell updates/sec

Title: US-10-624-932-1
Perfect score: 2752
Sequence: 1 ccgcggggccccgcgcccgg.....tgagtgctgaggccggccag 2752

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	960.2	34.9	2802	9	AY406491	AY406491 Homo sapi
2	950.4	34.5	2791	9	AY406493	AY406493 Mus muscu
3	923.4	33.6	3790	3	AK031655	AK031655 Mus muscu
4	884	32.1	1852	3	CR598115	CR598115 full-leng
5	872.4	31.7	3866	3	AK018177	AK018177 Mus muscu
6	814	29.6	2802	9	AY406492	AY406492 Pan trogl
7	810.4	29.4	2532	9	AY411747	AY411747 Homo sapi
8	780.4	28.4	2532	9	AY411749	AY411749 Mus muscu

9	768.6	27.9	1034	4	BI758231	BI758231	603029876
10	736.6	26.8	1532	3	BC033727	BC033727	Homo sapi
11	735.2	26.7	788	1	AI951556	AI951556	wv36f04.x
c 12	721.6	26.2	796	5	BX348193	BX348193	BX348193
13	716.4	26.0	818	4	BI818609	BI818609	603033362
14	692	25.1	853	5	BX364574	BX364574	BX364574
15	678.2	24.6	2532	9	AY411748	AY411748	Pan trogl
16	672.6	24.4	934	2	BF311804	BF311804	601897316
17	666	24.2	900	5	BX345406	BX345406	BX345406
18	665	24.2	859	2	BF311896	BF311896	601897733
19	645.2	23.4	977	5	BX345407	BX345407	BX345407
20	631.2	22.9	1072	5	BX422753	BX422753	BX422753
21	618.8	22.5	756	5	BU612387	BU612387	UI-M-EW0-
22	613.2	22.3	874	5	BQ689148	BQ689148	AGENCOURT
23	610.2	22.2	2775	9	AY401471	AY401471	Mus muscu
24	607	22.1	889	5	BQ691915	BQ691915	AGENCOURT
25	599	21.8	2775	9	AY401469	AY401469	Homo sapi
26	595.2	21.6	601	1	AL516580	AL516580	AL516580
27	589.4	21.4	604	2	BE314370	BE314370	601147261
28	566.6	20.6	678	6	CA749784	CA749784	UI-M-FD0-
29	561	20.4	1175	2	BF530640	BF530640	602071931
30	555.6	20.2	788	6	CA317532	CA317532	UI-M-FW0-
31	555	20.2	572	7	CR554569	CR554569	DKFZp459I
32	494.2	18.0	499	7	CR747398	CR747398	CR747398
33	486.2	17.7	548	5	BX452510	BX452510	BX452510
34	475.4	17.3	824	4	BI737024	BI737024	603360874
35	471.2	17.1	540	4	BI467799	BI467799	389583 MA
36	470.8	17.1	2507	9	AY401470	AY401470	Pan trogl
37	438.2	15.9	675	6	CA315487	CA315487	UI-M-FW0-
38	433	15.7	471	5	BX282095	BX282095	BX282095
39	428.4	15.6	1147	5	BU840446	BU840446	AGENCOURT
40	424	15.4	843	4	BG913440	BG913440	602811321
41	417.8	15.2	856	7	CN164143	CN164143	994266 MA
42	411.8	15.0	749	7	CF735417	CF735417	UI-M-HB0-
43	410.6	14.9	1111	4	BG298307	BG298307	602397080
44	409.8	14.9	751	7	CF735550	CF735550	UI-M-HB0-
45	408.8	14.9	460	2	BF443156	BF443156	260542 MA

ALIGNMENTS

RESULT 1
AY406491
LOCUS AY406491 2802 bp DNA linear GSS 15-DEC-2003
DEFINITION Homo sapiens UNC5C gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY406491
VERSION AY406491.1 GI:39762465
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2802)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

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            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 2802)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .2802
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ORIGIN

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  Best Local Similarity   61.3%;  Pred. No. 6.4e-192;
  Matches 1682;  Conservative    0;  Mismatches  995;  Indels   69;  Gaps    6;

Qy         57 GCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGG 116
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Db         66 GCTCGTGCTACCTGCCCTGGCCCTGCTCAGCGCCAGCGGCACTGGCTCCGCCGCCCAAGA 125

Qy        117 TGCCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCC 176
              ||   |      |       |  |  |  |  | ||| ||     || || |  || ||
Db        126 TGATGACTTTTTTCATGAACTCCCAGAAACTTTTCCTTCTGATCCACCTGAGCCTCTGCC 185

Qy        177 CCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGT 236
               || |||||  | |||||| || || |  || || || ||||| ||||| |||   ||
Db        186 ACATTTCCTTATTGAGCCTGAAGAAGCTTATATTGTGAAGAATAAGCCTGTGAACCTGTA 245

Qy        237 GTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCA 296
               || || ||    || ||||| |||||||  |||||||| ||  | || |||||  |  ||
Db        246 CTGTAAAGCAAGCCCTGCCACCCAGATCTATTTCAAGTGTAATAGTGAATGGGTTCATCA 305

Qy        297 GGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGT 356
              |  ||||||| |  | ||    ||   ||| |  |     || ||      |  ||| ||
Db        306 GAAGGACCACATAGTAGATGAAAGAGTAGATGAAACTTCCGGTCTCATTGTCCGGGAAGT 365

Qy        357 CCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCGGGCTGGAGGAATACTGGTG 416
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Db        366 GAGCATTGAGATTTCGCGCCAGCAAGTGGAAGAACTCTTTGGACCTGAAGATTACTGGTG 425

Qy        417 CCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCAT 476
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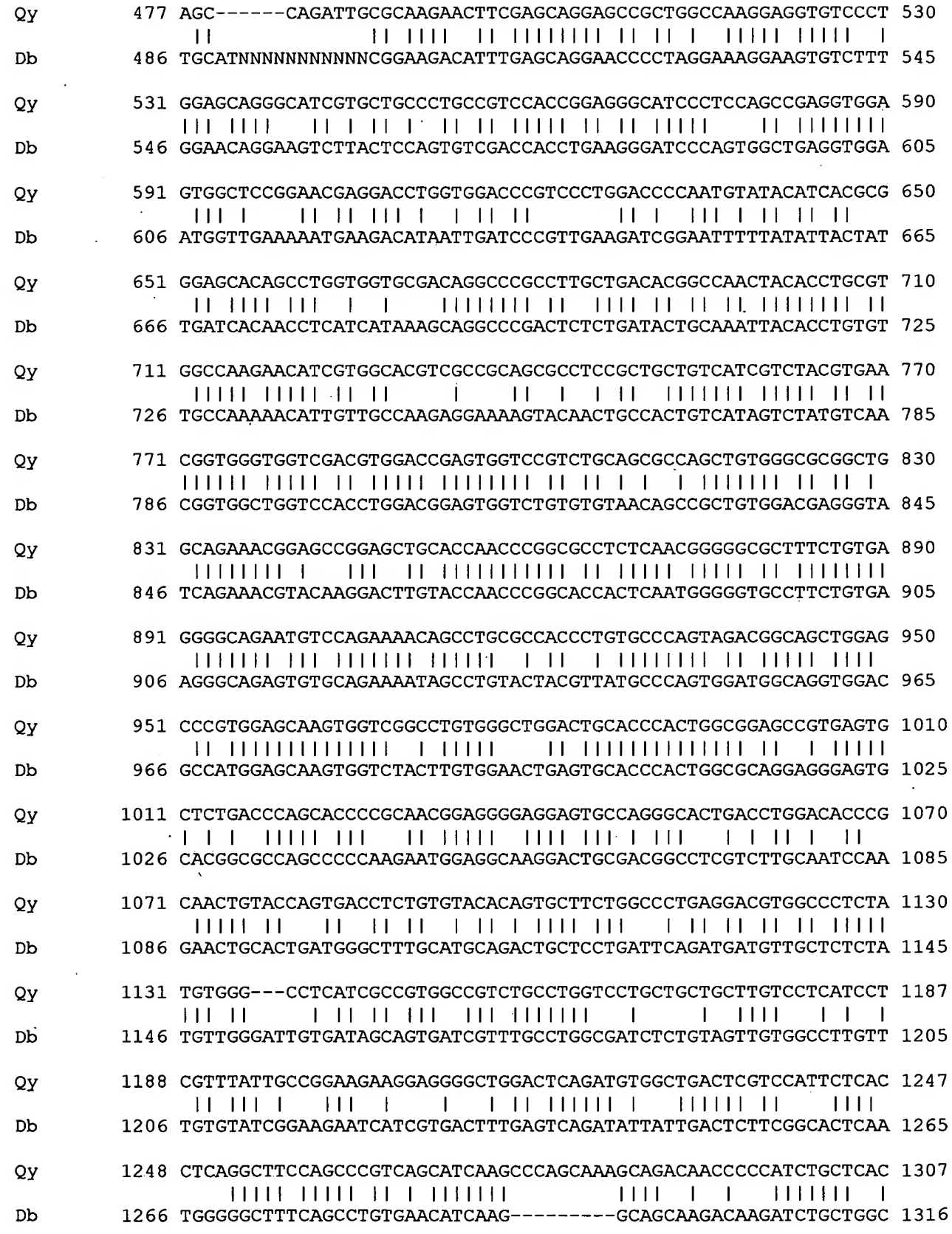

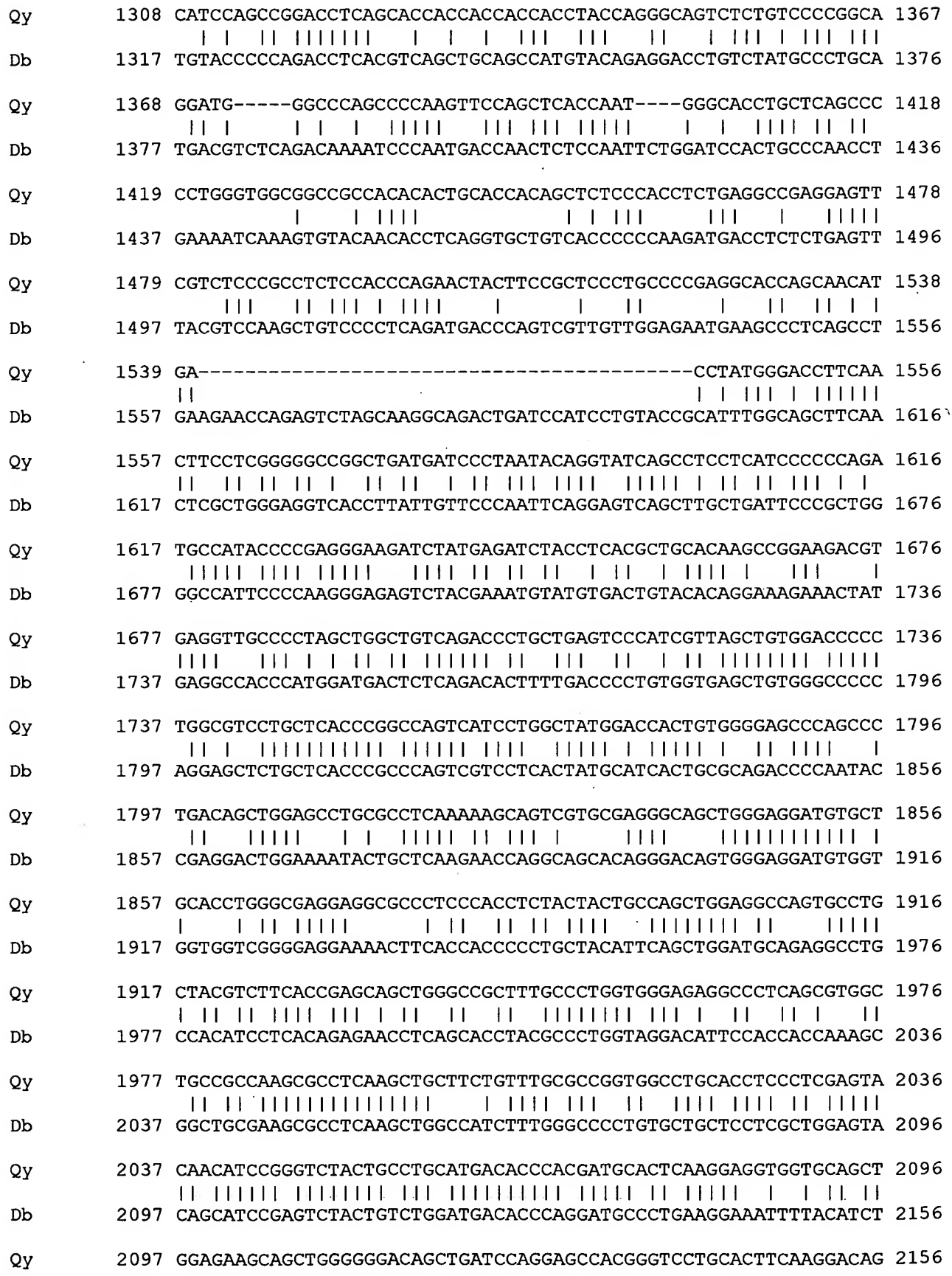

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Db       2217 CACCCACAACCTGCGCCTGTCAATTCACGATATCGCCCATTCCCTCTGGAAGAGCAAATT 2276

Qy       2217 CCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTT 2276

Db       2277 GCTGGCTAAATATCAGGAAATTCCATTTTACCATGTTTGGAGTGGATCTCAAAGAAACCT 2336

Qy       2277 GCACTGCACCTTCACCCTGGAGCGTGTCAGCCCCAGCACTAGTGACCTGGCCTGCAAGCT 2336

Db       2337 GCACTGCACCTTCACTCTGGAAAGATTTAGCCTGAACACAGTGGAGCTGGTTTGCAAACT 2396

Qy       2337 GTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAA 2396

Db       2397 CTGTGTGCGGCAGGTGGAAGGAGAAGGGCAGATCTTCCAGCTCAACTGCACCGTGTCAGA 2456

Qy       2397 GGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGT 2456

Db       2457 GGAACCTACTGGCATCGATTTGCCGCTGCTGGATCCTGCGAACACCATCACCACGGTCAC 2516

Qy       2457 GGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGA 2516

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Qy       2517 CCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAACTCCACCTGGACAG 2576

Db       2577 TGCCCCCCAGACGAGAGGCCATGACTGGAGGATGCTGGCCCATAAGCTGAACCTGGACAG 2636

Qy       2577 CCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGA 2636

Db       2637 GTACTTGAATTACTTTGCCACCAAATCCAGCCCAACTGGCGTAATCCTGGATCTTTGGGA 2696

Qy       2637 GGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGG 2696

Db       2697 AGCACAGAACTTCCCAGATGGAAACCTGAGCATGCTGGCAGCTGTCTTGGAAGAAATGGG 2756

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RESULT 2
AY406493

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LOCUS       AY406493                2791 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Mus musculus UNC5C gene, VIRTUAL TRANSCRIPT, partial sequence,
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ACCESSION   AY406493
VERSION     AY406493.1  GI:39762467
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 2791)
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  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 2791)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .2791
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
     gene            <1. .>2791
                     /gene="UNC5C"
                     /locus_tag="HCM2575"
ORIGIN

  Query Match             34.5%;  Score 950.4;  DB 9;  Length 2791;
  Best Local Similarity   62.3%;  Pred. No. 7.5e-190;
  Matches 1653;  Conservative    0;  Mismatches  921;  Indels   80;  Gaps    7;

Qy        149 TGCCTGGTGCCAACCCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACA 208
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Db        158 TTCCATCTGACCCACCTGAGCCATTGCCACACTTCCTCATTGAGCCCGAGGAAGCTTACA 217

Qy        209 TCGTCAAGAACAAGCCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCT 268
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Db        218 TTGTGAAGAACAAGCCTGTGAACCTGTATTGTAAAGCCAGCCCTGCCACCCAGATCTACT 277

Qy        269 TCAAGTGCAACGGGGAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACG 328
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Qy        329 GGAGCAGTGGGCTGCCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGA 388
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Db        338 AAACCTCTGGTCTAATTGTGAGAGAAGTGAGCATTGAGATTTCACGCCAGCAGGTGGAGG 397

Qy        389 AGGTGTTCGGGCTGGAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCA 448
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Db        398 AACTGTTTGGGCCTGAAGATTACTGGTGCCAGTGTGTGGCCTGGAGCTCAGCAGGCACTA 457

Qy        449 CCAAGAGTCAGAAGGCCTACATCCGCATAGCCAG------ATTGCGCAAGAACTTCGAGC 502
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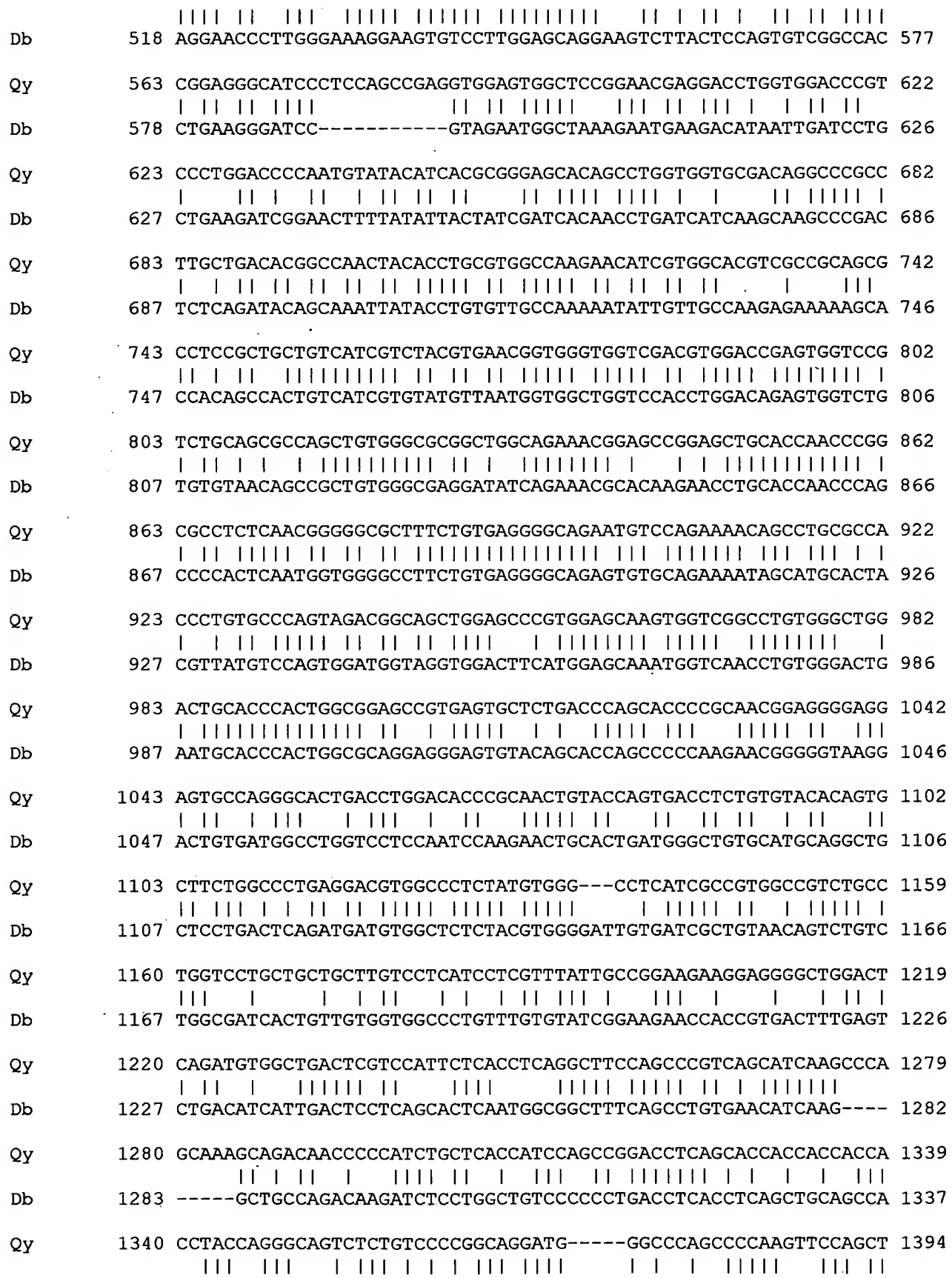

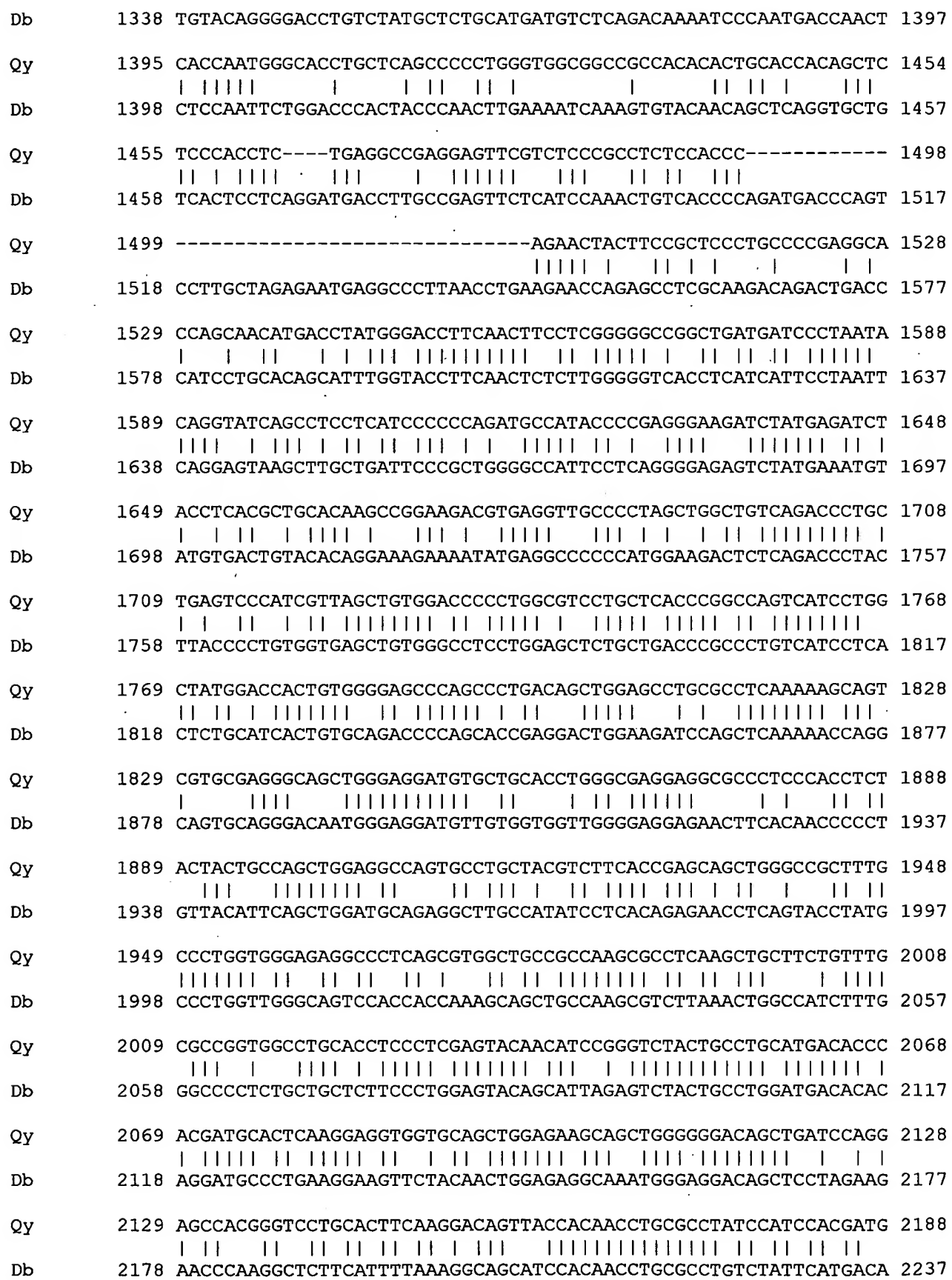

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Qy       2249 ACATCTGGAATGGCACGCAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTCAGCC 2308
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Qy       2309 CCAGCACTAGTGACCTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGA 2368
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Qy       2429 AGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCA 2488
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Qy       2489 TTCGGCAGAAGATAATTTCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGA 2548
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Qy       2549 CTCTGGCCCAGAAACTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCC 2608
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Qy       2609 CCACAGCCATGATCCTCAACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCC 2668
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Qy       2669 AGCTGGCTGCAGCAGTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTCGG 2728
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Qy       2729 AGGCTGAGTGCTGA 2742
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Db       2778 AAGGACAGTATTGA 2791
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RESULT 3
AK031655
LOCUS       AK031655               3790 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
            enriched library, clone:6030473H24 product:unc5 homolog (C.
            elegans) 3, full insert sequence.
ACCESSION   AK031655
VERSION     AK031655.1  GI:26327502
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
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TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3790)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

```
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
     source          1. .3790
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                     /dev_stage="13 days embryo"
     CDS             118. .2970
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                     RIAYLRKTFEQEPLGKEVSLEQEVLLQCRPPEGIPVAEVEWLKNEDIIDPAEDRNFYI
                     TIDHNLIIKQARLSDTANYTCVAKNIVAKRKSTTATVIVYVNGGWSTWTEWSVCNSRC
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                     PQDDLAEFSSKLSPQMTQSLLENEALNLKNQSLARQTDPSCTAFGTFNSLGGHLIIPN
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ORIGIN

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  Best Local Similarity   61.3%;  Pred. No. 3.9e-184;
  Matches 1659;  Conservative    0;  Mismatches  926;  Indels  120;  Gaps    6;

Qy        149 TGCCTGGTGCCAACCCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACA 208
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Db        275 TTCCATCTGACCCACCTGAGCCATTGCCACACTTCCTCATTGAGCCCGAGGAAGCTTACA 334

Qy        209 TCGTCAAGAACAAGCCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCT 268
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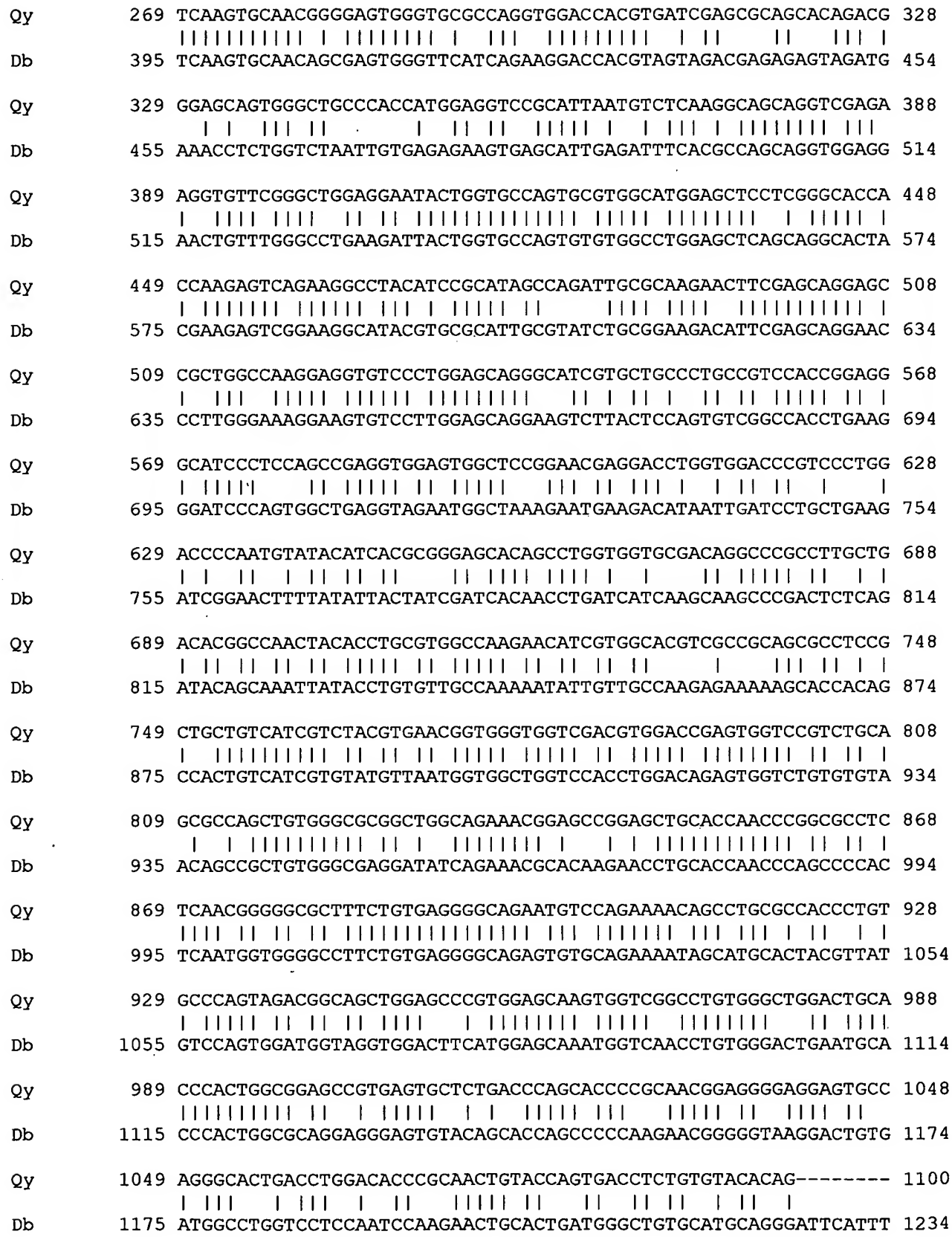

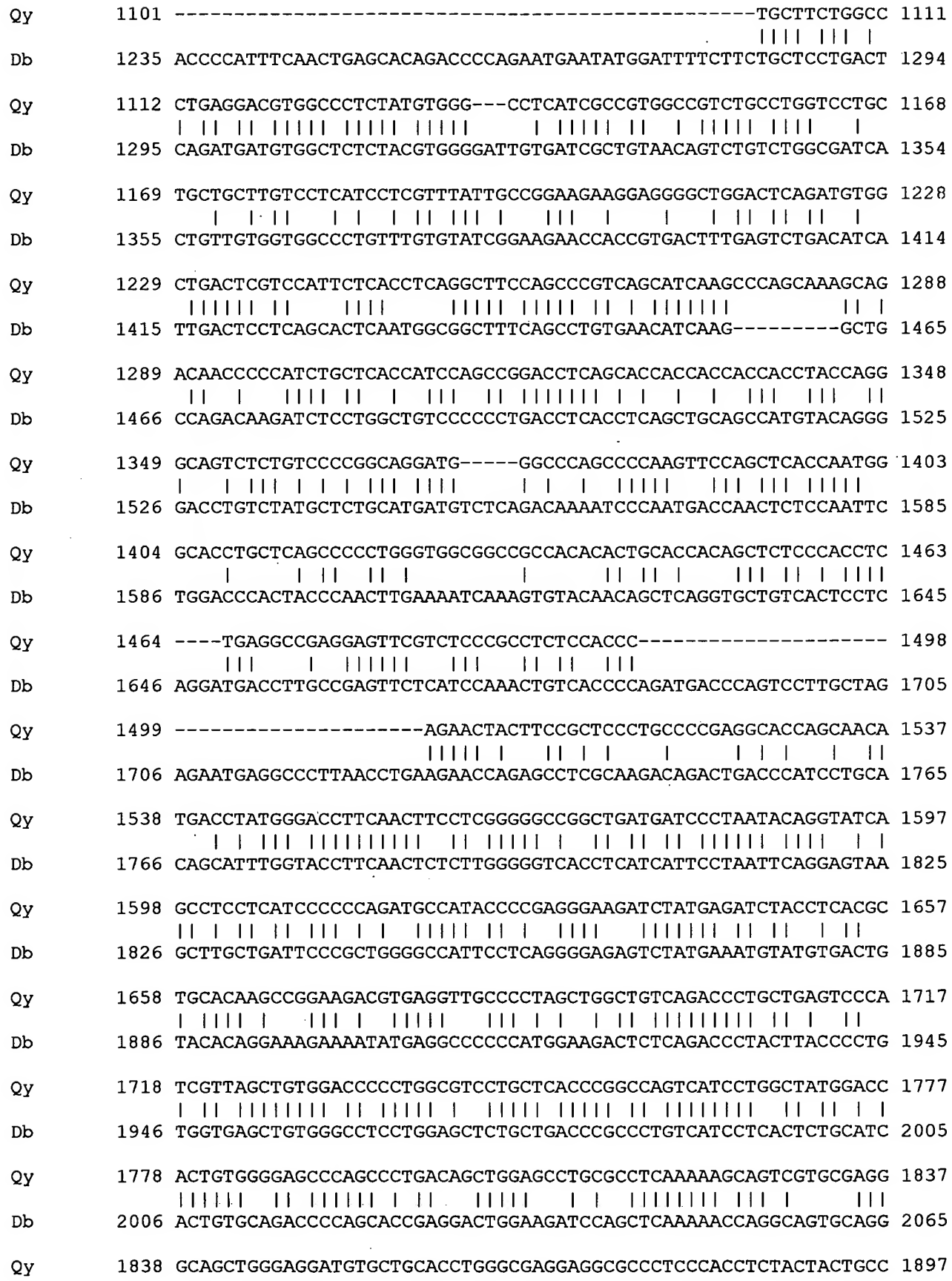

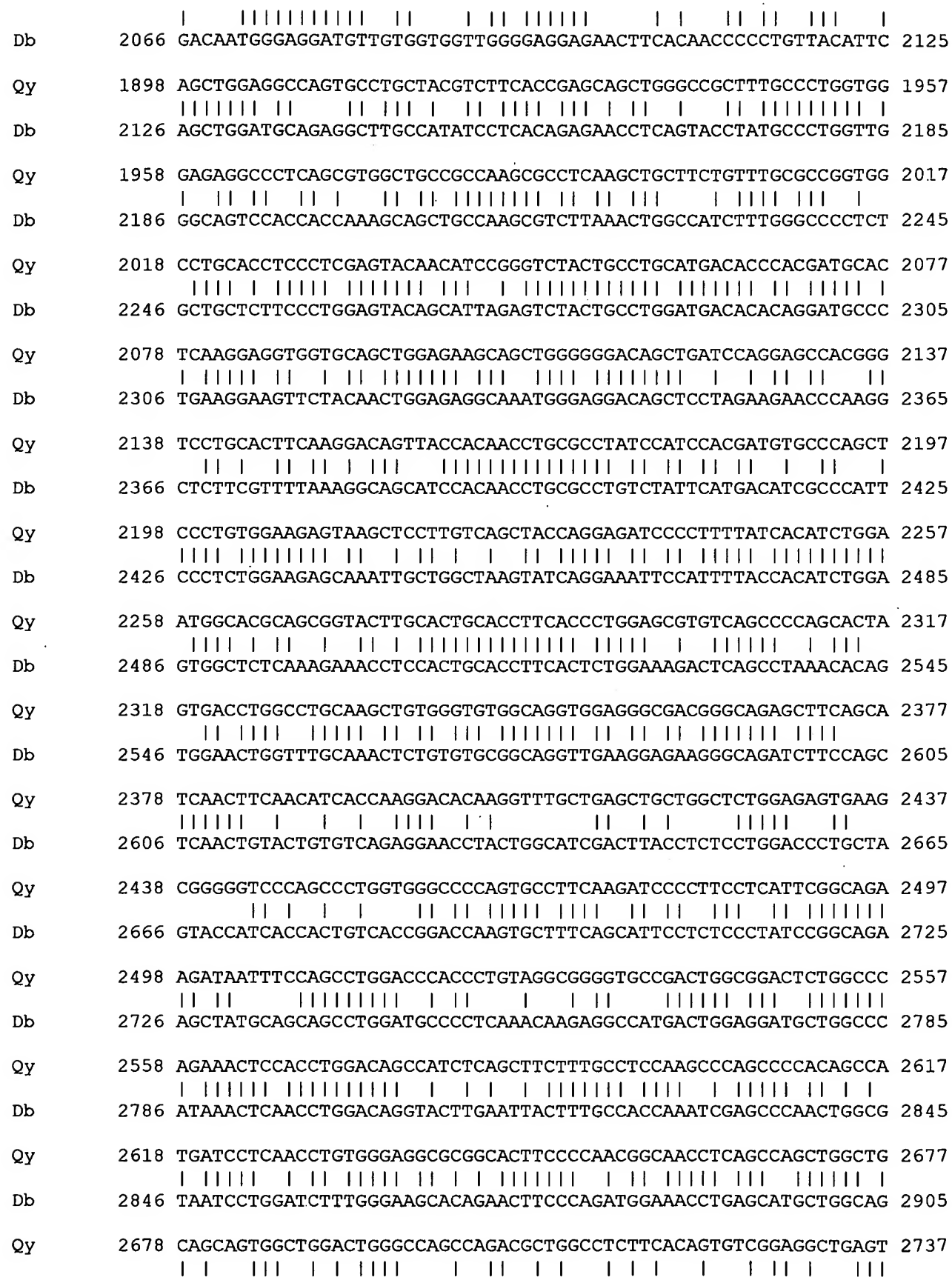

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Db       2906 CCGTCCTGGAAGAAATGGGAAGACATGAGACAGTGGTGTACTTGGCAGCAGAAGGACAGT 2965

Qy       2738 GCTGA 2742
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Db       2966 ATTGA 2970
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RESULT 4
CR598115

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LOCUS       CR598115                1852 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DA006YG16 of Neuroblastoma of Homo
            sapiens (human).
ACCESSION   CR598115
VERSION     CR598115.1  GI:50478922
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1852)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1852)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
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ORIGIN
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  Matches  884;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1869 GGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCAC 1928
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Db          1 GGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCAC 60

Qy       1929 CGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCG 1988
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Db         61 CGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCG 120

Qy       1989 CCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACATCCGGGT 2048
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Db        121 CCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACATCCGGGT 180

Qy       2049 CTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCT 2108
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Db        181 CTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCT 240

Qy       2109 GGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGACAGTTACCACAACCT 2168
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Db        241 GGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGACAGTTACCACAACCT 300

Qy       2169 GCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTTGTCAGCTA 2228
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Qy       2229 CCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCACTGCACCTT 2288
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Db        361 CCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCACTGCACCTT 420

Qy       2289 CACCCTGGAGCGTGTCAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGGGTGTGGCA 2348
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Qy       2349 GGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAGGACACAAGGTT 2408
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Db        481 GGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAGGACACAAGGTT 540

Qy       2409 TGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGCCCCAGTGC 2468
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Db        541 TGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGCCCCAGTGC 600

Qy       2469 CTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGACCCACCCTGTAG 2528
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Qy       2529 GCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAACTCCACCTGGACAGCCATCTCAGCTT 2588
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Db        721 CTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCGCGGCACTT 780

Qy       2649 CCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAGCCAGACGC 2708
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Qy       2709 TGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGAGGCCGGCCAG 2752
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RESULT 5
AK018177

LOCUS AK018177 3866 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330415E02 product:TRANSMEMBRANE RECEPTOR UNC5H2 homolog [Rattus norvegicus], full insert sequence.
ACCESSION AK018177
VERSION AK018177.1 GI:12857775
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3866)
AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,

Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT Please visit our web site (http://genome.gsc.riken.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.

FEATURES Location/Qualifiers

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/clone="6330415E02"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"

CDS 417. .3254
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AEGVIVYRRNCRDFDTDITDSSAALTGGFHPVNFKTARPNNPQLLHPSAPPDLTASAG
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GTYPGDFSRDTHFLHLRSASLGSQHLLGLPRDPSSSVSGTFGCLGGRLSLPGTGVSLL
VPNGAIPQGKFYDLYLHINKAESTLPLSEGSQTVLSPSVTCGPTGLLLCRPVVLTVPH
CAEVIAGDWIFQLKTQAHQGHWEEVVTLDEETLNTPCYCQLEAKSCHILLDQLGSYVF
MGESYSRSAVKRLQLAIFAPALCTSLEYSLRVYCLEDTPVALKEVLELERTLGGYLVE
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ORIGIN

Query Match 31.7%; Score 872.4; DB 3; Length 3866;
Best Local Similarity 60.6%; Pred. No. 2.3e-173;
Matches 1646; Conservative 0; Mismatches 941; Indels 129; Gaps 8;

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Qy        157 GCCAACCCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAG 216
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Qy        217 AACAAGCCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGC 276
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Db        660 AATGGCGAGTGGGTCAGCCAGAATGACCACGTCACACAGGAGAGCCTGGATGAGGCCACA 719

Qy        337 GGGCTGCCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTC 396
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Qy        517 AAGGAGGTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCT 576
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Qy        577 CCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAAT 636
                 ||  ||||||||  ||||||  |||  ||  ||   |  |  |||||  |  |  ||||  |  ||
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Qy        637 GTATACATCACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCC 696
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Db       1080 AACTACACCTGTGTGGCCAAGAATATCGTGGCCAAGCGCCGGAGCACCGCGGCCACAGTC 1139

Qy        757 ATCGTCTACGTGAACGGTGGGTGGTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGC 816
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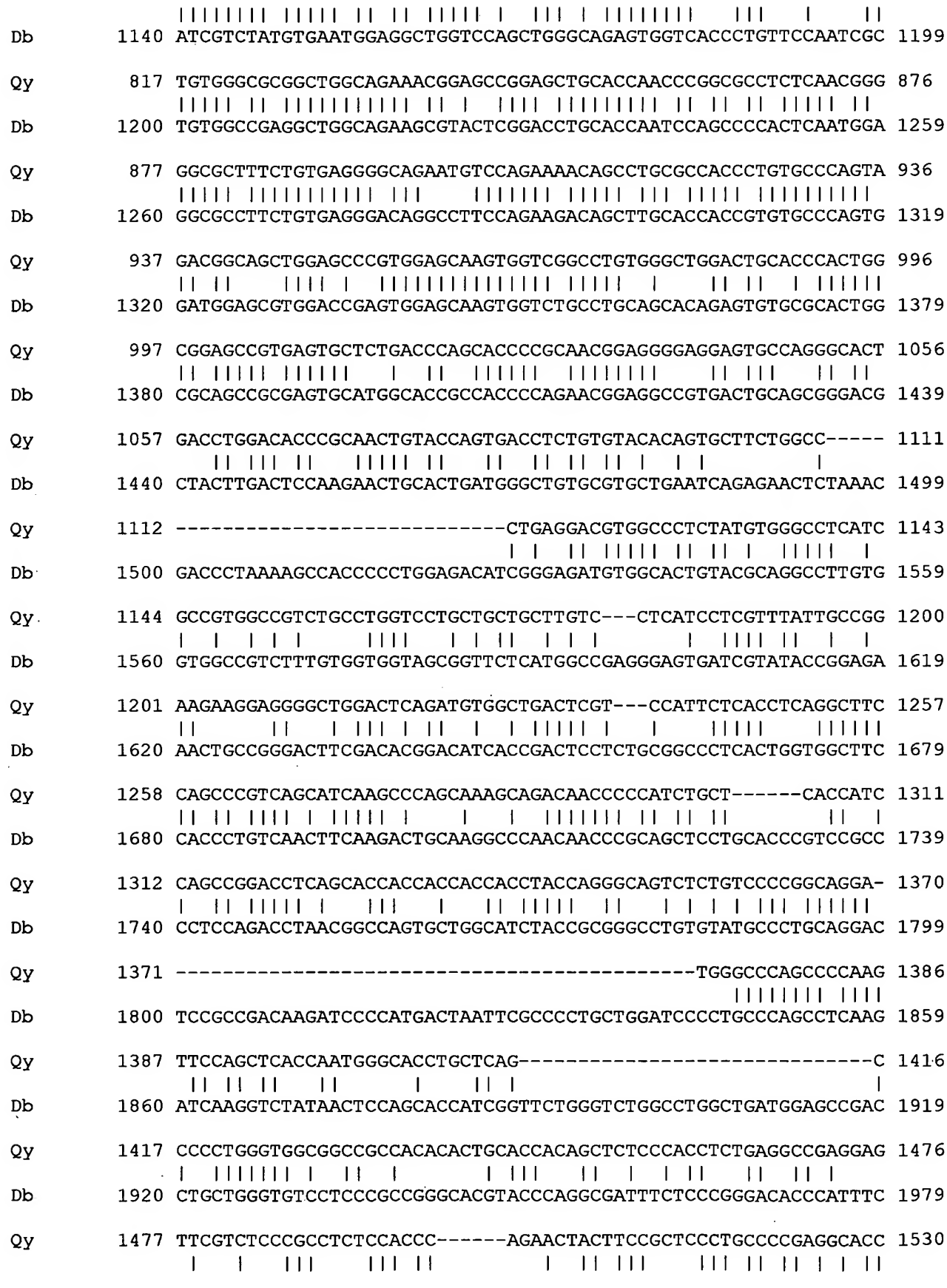

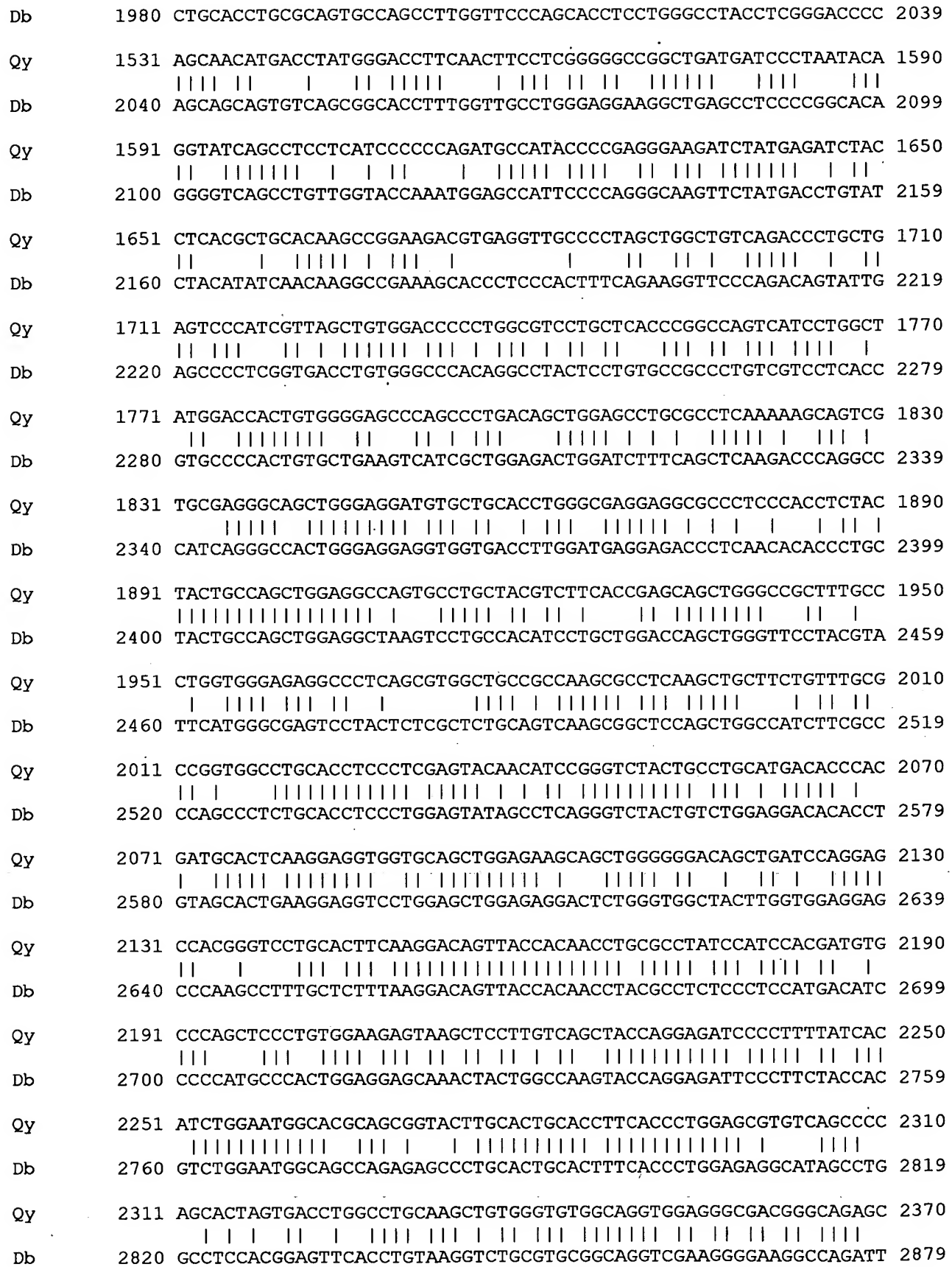

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Qy       2428 GAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTC 2487
Db       2940 GCCCCGGGCAATGCCATCACCACCCAGCTGGGACCCTATGCCTTCAAGATACCCCTGTCC 2999

Qy       2488 ATTCGGCAGAAGATAATTTCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGG 2547
Db       3000 ATCCGCCAAAAGATCTGCAGCAGCCTGGACGCCCCCGACTCCCGGGGCAACGACTGGAGG 3059

Qy       2548 ACTCTGGCCCAGAAACTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGC 2607
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Qy       2608 CCCACAGCCATGATCCTCAACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGC 2667
Db       3120 CCCACAGGTGTCATCTTAGACCTCTGGGAAGCTCGGCAACAGGATGACGGGGACCTCAAC 3179

Qy       2668 CAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTCG 2727
Db       3180 AGCCTGGCCAGTGCCTTGGAGGAGATGGGCAAGAGTGAGATGCTGGTAGCCATGGCCACA 3239

Qy       2728 GAGGCTGAGTGCTGAG 2743
Db       3240 GATGGCGATTGCTGAG 3255
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RESULT 6
AY406492
LOCUS AY406492 2802 bp DNA linear GSS 15-DEC-2003
DEFINITION Pan troglodytes UNC5C gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY406492
VERSION AY406492.1 GI:39762466
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 2802)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2802)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission

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  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
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ORIGIN

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  Matches 1477;  Conservative    0;  Mismatches 1200;  Indels   69;  Gaps    6;

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Qy        117 TGCCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCC 176
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Db        126 TGATGACTTTTTTCATGAACTCCCAGAAACTTTTCCTTCGGATCCACCTGAGCCTCTGCC 185

Qy        177 CCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGT 236
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Db        186 ACATTTCCTTATTGAACCTGAGGAAGCTTATATTGTGAAGAATAAGCCTGTGAACCTGTA 245

Qy        237 GTGCAAGGCC------GTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGT 290
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Db        246 CTGTAAAGCAAGCCCTGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 305

Qy        291 GCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCAT 350

Db        306 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 365

Qy        351 GGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCGGGCTGGAGGAATA 410

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Db        546 GGAACAGGAAGTCTTACTCCAGTGTCGGCCACCTGAAGGGATCCCAGTGGCTGAGNNNNN 605

Qy        591 GTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCG 650
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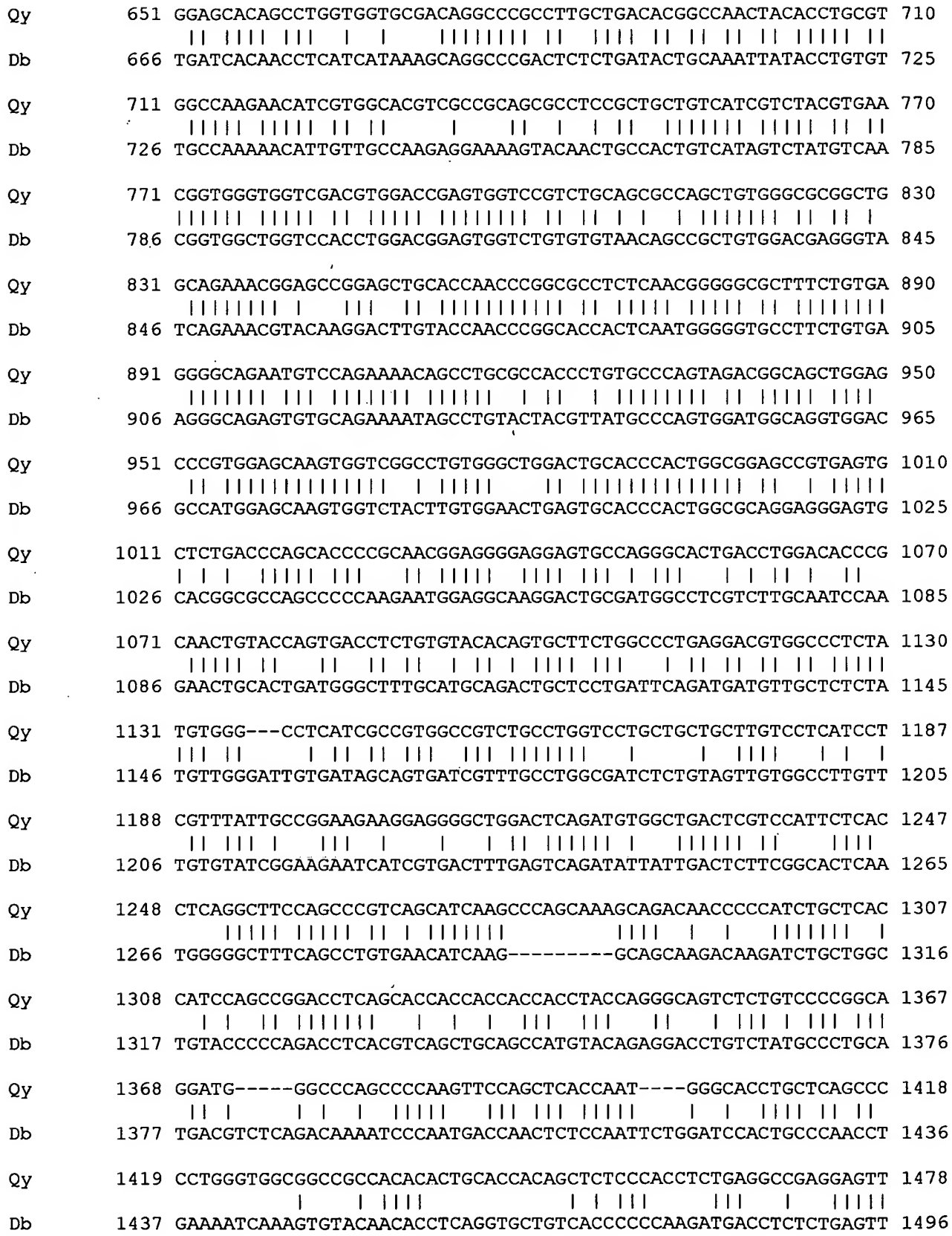

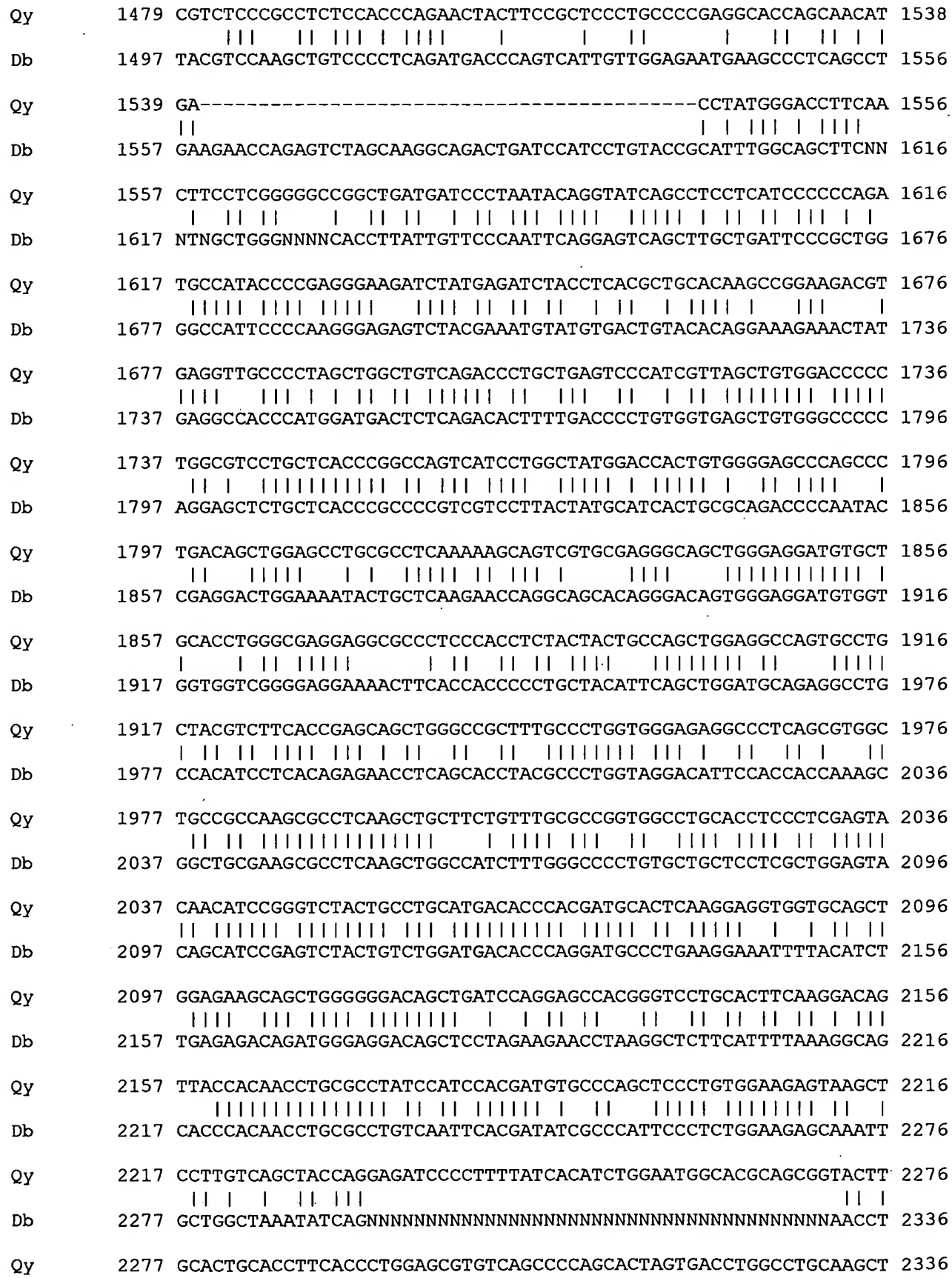

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Qy       2337 GTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAA 2396
               || ||| |||||||||| || || ||||||| ||||    |||||| || | |  |  |
Db       2397 CTGTGTGCGGCAGGTGGAAGGAGAAGGGCAGATCTTCCAGCTCAACTGCACCGTGTCAGA 2456

Qy       2397 GGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGT 2456
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Db       2457 GGAACCTACTGGCATCGATTTGCCGCTGCTGGATCCTGCGAACACCATCACCACGGTCAC 2516

Qy       2457 GGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGA 2516
               ||| |||||||| ||||  |||||  |||  || |||||||||  |   |  |||||||||
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Qy       2517 CCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAACTCCACCTGGACAG 2576
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Db       2577 TGCCCCCCAGACGAGAGGCCATGACTGGAGGATGCTGGCCCATAAGCNNNNNNNNNNNNN 2636

Qy       2577 CCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGA 2636
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Db       2637 GTACTTGAATTACTTTGCCACCAAATCCAGCCCAACTGGCGTAATCCTGGATCTTTGGGA 2696

Qy       2637 GGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGG 2696
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Db       2697 AGCACAGAACTTCCCAGATGGAAACCTGAGCATGCTGGCAGCTGTCTTGGAAGAAATGGG 2756

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RESULT 7
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DEFINITION  Homo sapiens HCM4327 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY411747
VERSION     AY411747.1  GI:39767715
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2532)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 2532)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
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            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
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Query Match 29.4%; Score 810.4; DB 9; Length 2532;
Best Local Similarity 61.1%; Pred. No. 2.7e-160;
Matches 1540; Conservative 0; Mismatches 851; Indels 129; Gaps 9;

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Db         73 TGGTGCCAGTGCGTGGCCTGGAGCTCCGCGGGCACCACCAAGAGTCGCCGAGCCTACGTC 132

Qy        472 CGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTG 531
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Db        133 CGCATCGCCTACCTGCGCAAGAACTTCGATCAGGAGCCTCTGGGCAAGGAGGTGCCCCTG 192

Qy        532 GAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAG 591
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Db        193 GACCATGAGGTTCTCCTGCAGTGCCGCCCGCCGGAGGGGGTGCCTGTGGCCGAGGTGGAA 252

Qy        592 TGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGG 651
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Db        253 TGGCTCAAGAATGAGGATGTCATCGACCCCACCCAGGACACCAACTTCCTGCTCACCATC 312

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Db        313 GACCACAACCTCATCATCCGCCAGGCCCGCCTGTCGGACACTGCCAACTATACCTGCGTG 372

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Db        373 GCCAAGAACATCGTGGCCAAACGCCGGAGCACCACTGCCACCGTCATCGTCTACGTGAAT 432

Qy        772 GGTGGGTGGTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGG 831
              ||  ||  |||||  |  |||  |  ||||||||   ||||  |  |  |||||||  ||  ||||||
Db        433 GGCGGCTGGTCCAGCTGGGCAGAGTGGTCACCCTGCTCCAACCGCTGTGGCCGAGGCTGG 492

Qy        832 CAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAG 891
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Db        493 CAGAAGCGCACCCGGACCTGCACCAACCCCGCTCCACTCAACGGAGGGGCCTTCTGCGAG 552

Qy        892 GGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGCTGGAGC 951
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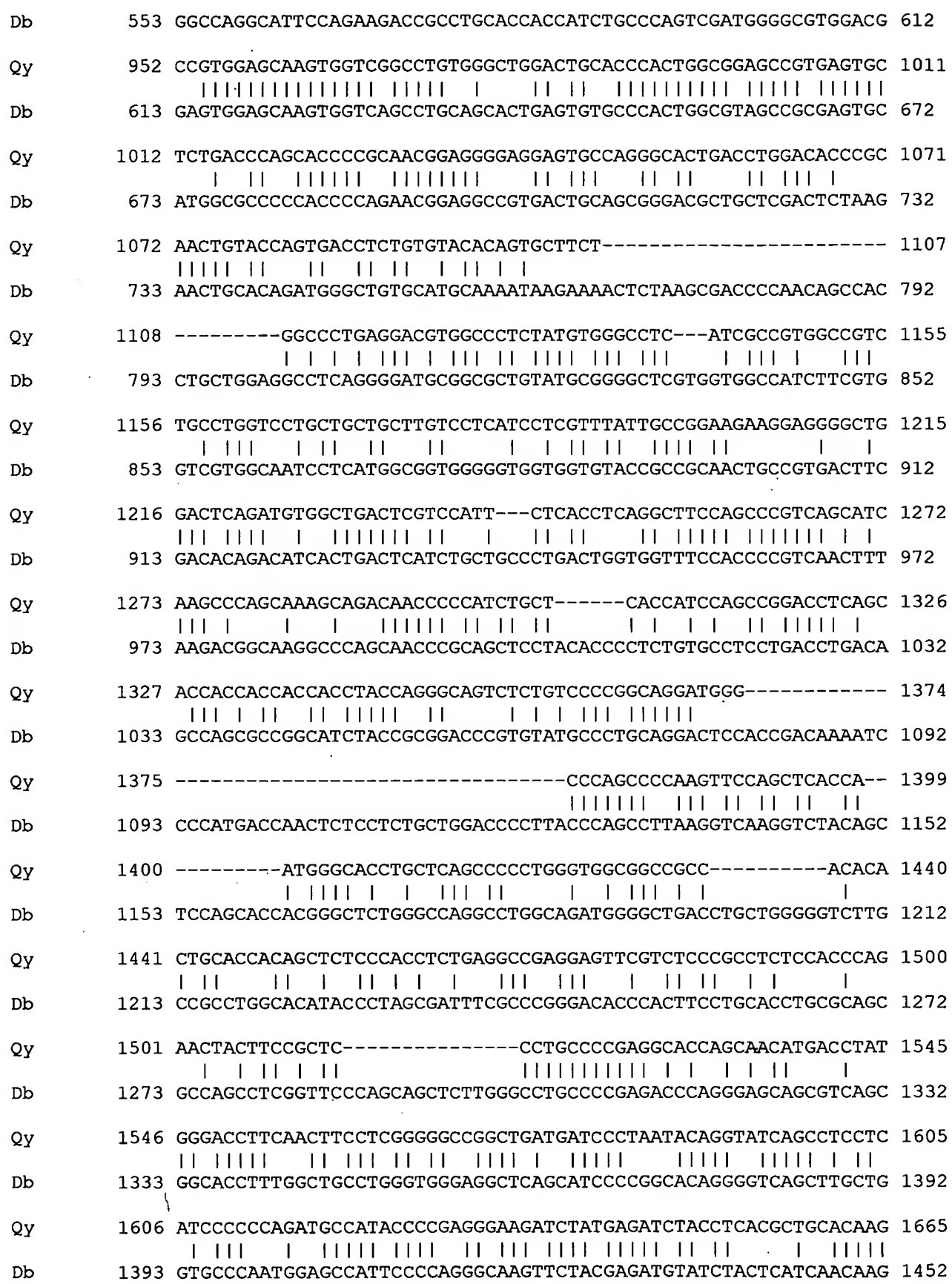

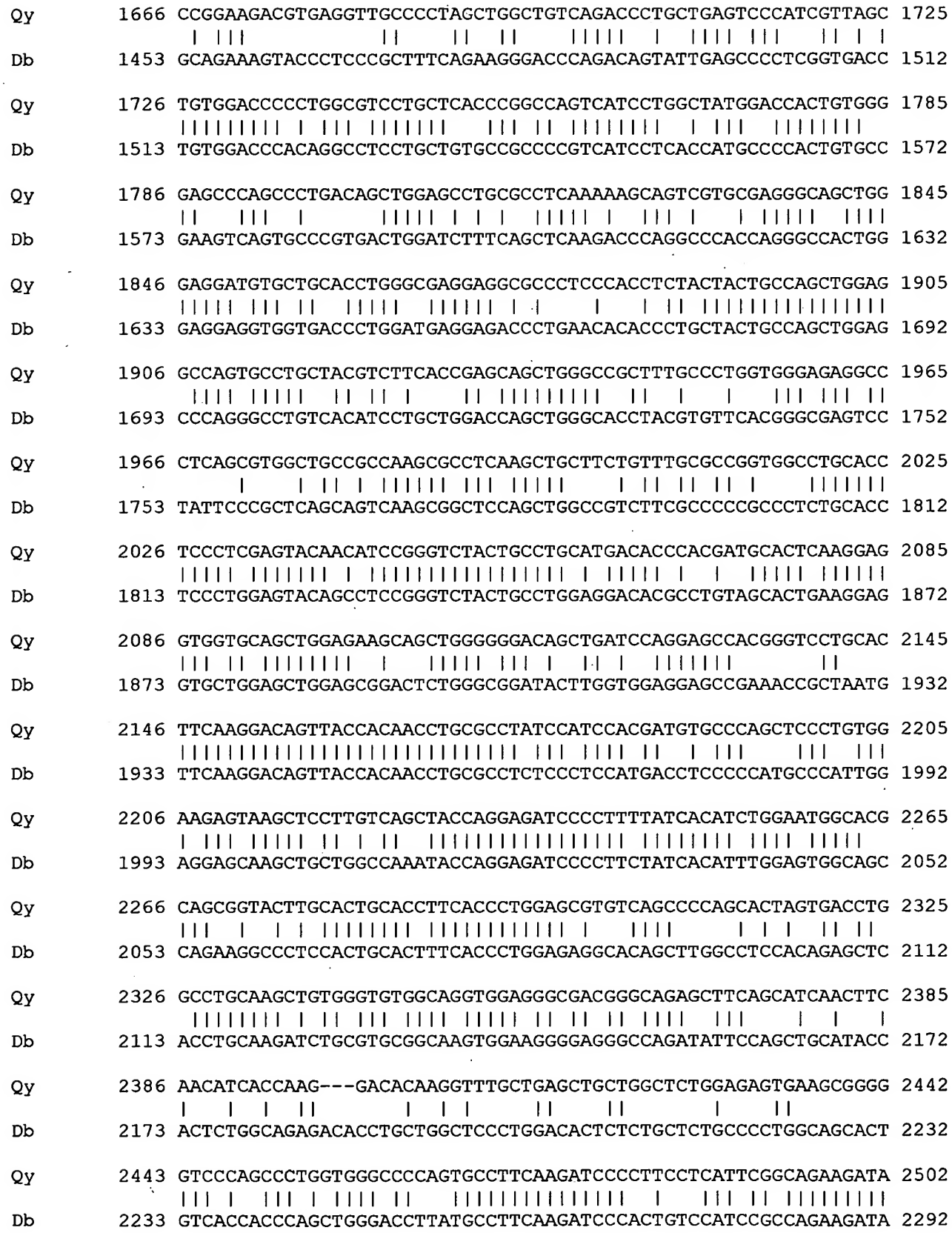
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Qy 1726 TGTGGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGG 1785
Db 1513 TGTGGACCCACAGGCCTCCTGCTGTGCCGCCCCGTCATCCTCACCATGCCCCACTGTGCC 1572
Qy 1786 GAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG 1845
Db 1573 GAAGTCAGTGCCCGTGACTGGATCTTTCAGCTCAAGACCCAGGCCCACCAGGGCCACTGG 1632
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Db 1633 GAGGAGGTGGTGACCCTGGATGAGGAGACCCTGAACACACCCTGCTACTGCCAGCTGGAG 1692
Qy 1906 GCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCC 1965
Db 1693 CCCAGGGCCTGTCACATCCTGCTGGACCAGCTGGGCACCTACGTGTTCACGGGCGAGTCC 1752
Qy 1966 CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC 2025
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Qy 2086 GTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCAC 2145
Db 1873 GTGCTGGAGCTGGAGCGGACTCTGGGCGGATACTTGGTGGAGGAGCCGAAACCGCTAATG 1932
Qy 2146 TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGG 2205
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Qy 2206 AAGAGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACG 2265
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Qy 2266 CAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTCAGCCCCAGCACTAGTGACCTG 2325
Db 2053 CAGAAGGCCCTCCACTGCACTTTCACCCTGGAGAGGCACAGCTTGGCCTCCACAGAGCTC 2112
Qy 2326 GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTC 2385
Db 2113 ACCTGCAAGATCTGCGTGCGGCAAGTGGAAGGGGAGGGCCAGATATTCCAGCTGCATACC 2172
Qy 2386 AACATCACCAAG---GACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGG 2442
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Qy 2443 GTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATA 2502
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Db       2353 CTCTCTATGGACCGGTACCTGAATTACTTTGCCACCAAAGCGAGCCCCACGGGTGTGATC 2412

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LOCUS       AY411749                2532 bp    DNA     linear   GSS 12-DEC-2003
DEFINITION  Mus musculus HCM4327 gene, VIRTUAL TRANSCRIPT, partial sequence,
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ACCESSION   AY411749
VERSION     AY411749.1  GI:39767717
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 2532)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 2532)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
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Query Match 28.4%; Score 780.4; DB 9; Length 2532;
Best Local Similarity 60.1%; Pred. No. 5.8e-154;
Matches 1515; Conservative 0; Mismatches 876; Indels 129; Gaps 8;

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Qy        352 GAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCGGGCTGGAGGAATAC 411
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Db         13 GAGGTGCAGATCGAGGTGTCACGGCAGCAAGTGGAGGAACTCTTCGGGCTCGAGGACTAC 72

Qy        412 TGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATC 471
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Db         73 TGGTGCCAGTGCGTGGCCTGGAGCTCTTCGGGAACTACCAAGAGTCGCCGAGCCTACATC 132

Qy        472 CGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTG 531
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Db        133 CGCATTGCCTACTTGCGCAAGAACTTTGACCAGGAGCCTCTGGCCAAGGAGGTACCCTTG 192

Qy        532 GAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAG 591
              || || |   || | ||||  ||||| ||||||||||  | |||   || ||||||||
Db        193 GATCATGAGGTCCTTCTGCAGTGCCGCCCACCGGAGGGAGTGCCTGTGGCTGAGGTGGAA 252

Qy        592 TGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGG 651
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Db        253 TGGCTCAAGAATGAAGATGTCATTGACCCCGCTCAGGACACTAACTTCCTGCTCACCATT 312

Qy        652 GAGCACAGCCTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGTG 711
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Db        313 GACCACAACCTCATCATCCGCCAGGCGCGCCTCTCAGACACGGCCAACTACACCTGTGTG 372

Qy        712 GCCAAGAACATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTCATCGTCTACGTGAAC 771
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Db        373 GCCAAGAATATCGTGGCCAAGCGCCGGAGCACCACGGCCACAGTCATCGTCTATGTGAAT 432

Qy        772 GGTGGGTGGTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGG 831
              || || ||||| |  ||| | ||||||||   |||   |    ||||||| || ||||||
Db        433 GGAGGCTGGTCCAGCTGGGCAGAGTGGTCACCCTGTTCCAATCGCTGTGGCCGAGGCTGG 492

Qy        832 CAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAG 891
              ||||| || |  |||| ||||||||| || || || ||||| || ||||| |||||||||
Db        493 CAGAAGCGTACTCGGACCTGCACCAATCCAGCCCCACTCAATGGAGGCGCCTTCTGTGAG 552

Qy        892 GGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGCTGGAGC 951
              || |||    ||||||| ||||| ||| ||||| |||||||||| || ||    |||| |
Db        553 GGACAGGCCTTCCAGAAGACAGCTTGCACCACCGTGTGCCCAGTGGATGGAGCGTGGACC 612

Qy        952 CCGTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGC 1011
                |||||||||||||||| |||||  |    || ||  | |||||||| ||||| ||||||
Db        613 GAGTGGAGCAAGTGGTCTGCCTGCAGCACAGAGTGTGCGCACTGGCGCAGCCGCGAGTGC 672

Qy       1012 TCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGC 1071
                |  ||  ||||||  ||||||||    || |||   || ||    || ||| ||
Db        673 ATGGCACCGCCACCCCAGAACGGAGGCCGTGACTGCAGCGGGACGCTACTTGACTCCAAG 732

Qy       1072 AACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGAC---------- 1119
              |||||  ||   ||  || || || |  | |          |   | |||
Db        733 AACTGCACTGATGGGCTGTGCGTGCTGAATCAGAGAACTCTAAACGACCCTAAAAGCCAC 792

Qy       1120 ----------------------GTGGCCCTCTATGTGGGCCTCATCGCCGTGGCCGTCTGC 1158
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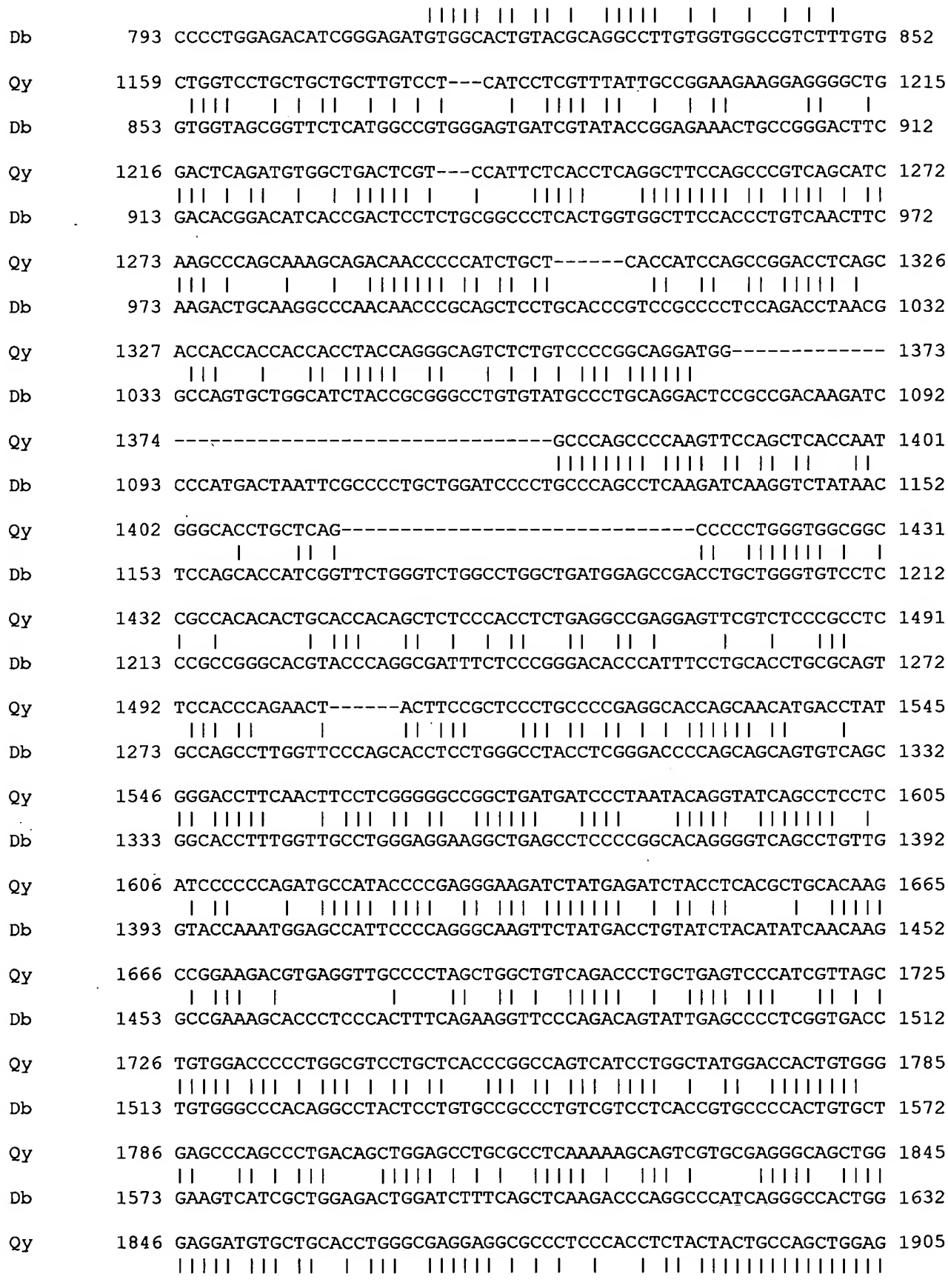

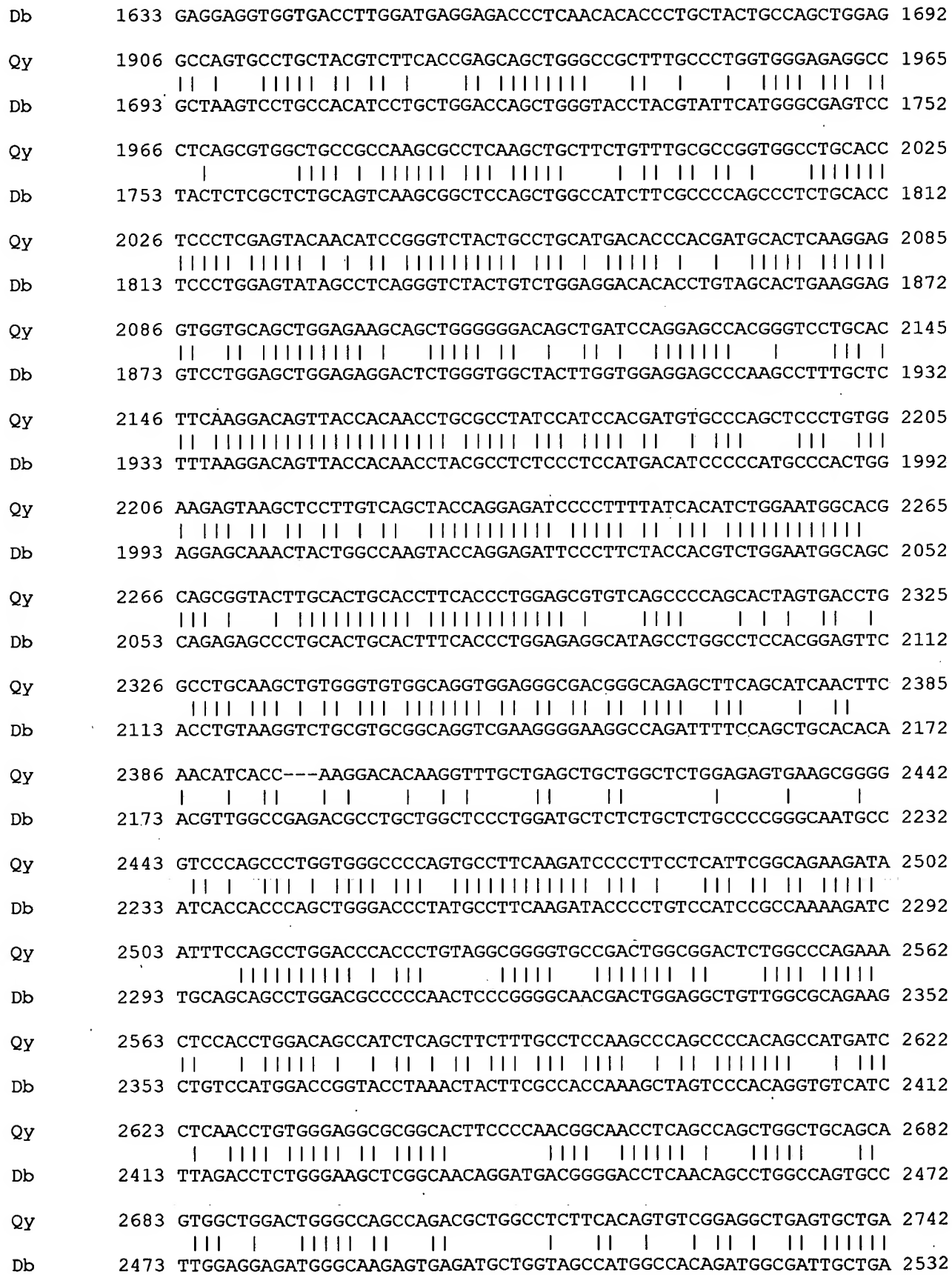

RESULT 9
BI758231
LOCUS BI758231 1034 bp mRNA linear EST 25-SEP-2001
DEFINITION 603029876F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5200171 5', mRNA sequence.
ACCESSION BI758231
VERSION BI758231.1 GI:15749809
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1034)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11501 row: g column: 20
High quality sequence stop: 793.
FEATURES Location/Qualifiers
source 1. .1034
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5200171"
/lab_host="DH10B"
/clone_lib="NIH_MGC_114"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."
ORIGIN

Query Match 27.9%; Score 768.6; DB 4; Length 1034;
Best Local Similarity 91.2%; Pred. No. 1.6e-151;
Matches 918; Conservative 0; Mismatches 74; Indels 15; Gaps 9;

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Qy        150 GCCTGGTGCCAACCCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACAT 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCCTGGTGCCAACCCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACAT 60

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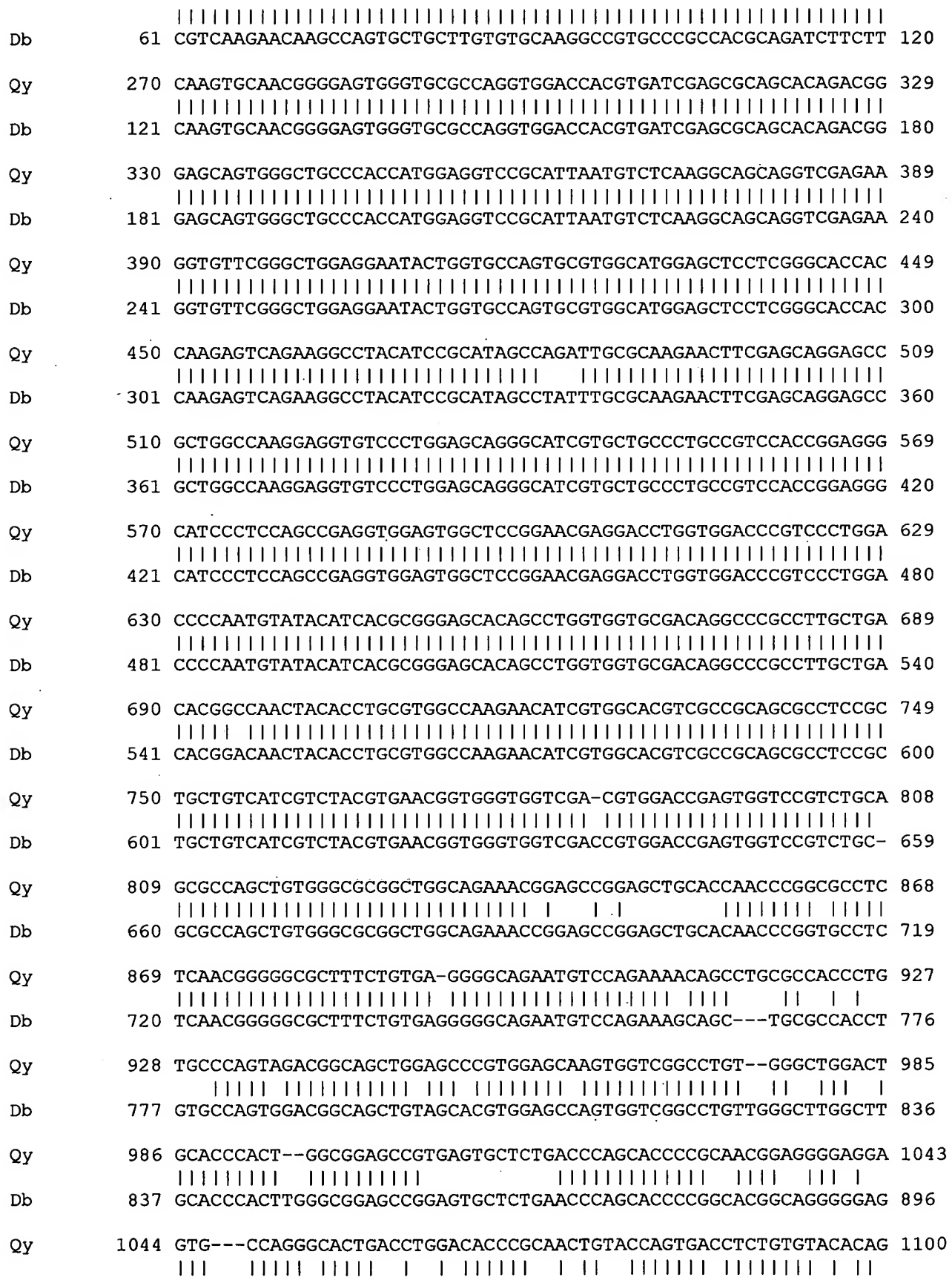

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Db        897 GTGTGCCCAGGTCACTGGACCTGGCACCCGGGA-TGGTCCAGTGAGCTCTGTGT-CCCAC 954

Qy       1101 TGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTCATCGCCG 1147
              | ||||||||||||||||| |||||  |||||||||||||||| | |
Db        955 GGGTTCTGGCCCTGAGGACTTGGCCTCCTATGTGGGCCTCATCCCGG 1001
```

RESULT 10
BC033727

```
LOCUS       BC033727               1532 bp    mRNA    linear   HTC 25-MAR-2004
DEFINITION  Homo sapiens unc-5 homolog A (C. elegans), mRNA (cDNA clone
            IMAGE:5166762), containing frame-shift errors.
ACCESSION   BC033727
VERSION     BC033727.1  GI:21707230
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1532)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1532)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUL-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
```

Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 68 Row: i Column: 2
This clone was selected for full length sequencing because it
passed the following selection criteria: GenomeScan gene prediction
This clone has the following problem: frame shifted.

FEATURES Location/Qualifiers
source 1. .1532
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5166762"
/tissue_type="Brain, adult medulla"
/clone_lib="NIH_MGC_119"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 26.8%; Score 736.6; DB 3; Length 1532;
Best Local Similarity 84.2%; Pred. No. 9.7e-145;
Matches 917; Conservative 0; Mismatches 4; Indels 168; Gaps 1;

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Qy        337 GGGCTGCCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTC 396
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        612 GGGCTGCCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTC 671

Qy        397 GGGCTGGAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGT 456
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        672 GGGCTGGAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGT 731

Qy        457 CAGAAGGCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCC 516
              |||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        732 CAGAAGGCCTACATCCGCATAGCCTATTTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCC 791

Qy        517 AAGGAGGTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCT 576
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        792 AAGGAGGTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCT 851

Qy        577 CCAGCCGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAAT 636
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        637 GTATACATCACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCC 696
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Db        912 GTATACATCACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCC 971
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Qy        697 AACTACACCTGCGTGGCCAAGAACATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTC 756
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Qy        757 ATCGTCTACGTGAACGGTGGGTGGTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGC 816
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Db       1032 ATCGTCTACGTG---------------------------------------------- 1043

Qy        817 TGTGGGCGCGGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGG 876

Db       1044 ---------------------------------------------------------- 1043

Qy        877 GGCGCTTTCTGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTA 936

Db       1044 ---------------------------------------------------------- 1043

Qy        937 GACGGCAGCTGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGG 996
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Db       1044 GACGGCAGCTGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGG 1103

Qy        997 CGGAGCCGTGAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACT 1056
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Qy       1057 GACCTGGACACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAG 1116
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Qy       1117 GACGTGGCCCTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTT 1176
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Qy       1177 GTCCTCATCCTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCG 1236
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Qy       1237 TCCATTCTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCC 1296
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Db       1344 TCCATTCTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCC 1403

Qy       1297 CATCTGCTCACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTC 1356
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Db       1404 CATCTGCTCACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTC 1463

Qy       1357 TGTCCCCGGCAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGC 1416
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Db       1464 TGTCCCCGGCAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGC 1523

Qy       1417 CCCCTGGGT 1425
              |||||||||
Db       1524 CCCCTGGGT 1532
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RESULT 11
AI951556
LOCUS AI951556 788 bp mRNA linear EST 09-MAR-2000

DEFINITION wv36f04.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531647 3' similar to TR:O08721 O08721 TRANSMEMBRANE RECEPTOR UNC5H1. ;, mRNA sequence.
ACCESSION AI951556
VERSION AI951556.1 GI:5743866
KEYWORDS EST.
SOURCE Homo sapiens (human)
  ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 788)
  AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
  JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center
  Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
  Insert Length: 1125 Std Error: 0.00
  Seq primer: -40UP from Gibco
  High quality sequence stop: 446.
FEATURES Location/Qualifiers
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  /lab_host="DH10B (phage-resistant)"
  /clone_lib="NCI_CGAP_Ov18"
  /note="Organ: ovary; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGCGACATTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "
ORIGIN

Query Match 26.7%; Score 735.2; DB 1; Length 788;
Best Local Similarity 96.5%; Pred. No. 1.8e-144;
Matches 749; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

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              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db          1 CCGAGGAGTTCGTCTCCCGCCTCTCCGCCCAGAACTACTTCCGCTCCCTGCCCCGAGGCA 60

Qy       1529 CCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATA 1588
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Db          61 CCAGCAACATGACCTATGGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATA 120

Qy        1589 CAGGTATCAGCCTCCTCATCCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCT 1648
                |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        1649 ACCTCACGCTGCACAAGCCGGAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGC 1708
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Qy        1709 TGAGTCCCATCGTTAGCTGTGGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGG 1768
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 CGTGCGAGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCT 420

Qy        1889 ACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTG 1948
                |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||| ||
Db         421 ACTACTGCCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGAGCCGCTATG 480

Qy        1949 CCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTG 2008
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Db         481 CCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTG 540

Qy        2009 CGCCGGTGGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCC 2068
                |||||||||||||||||||||||||||||||| | |||||||||||||||||||| |
Db         541 CGCCGGTGGCCTGCACCTCCCTCGAGTACAACATACTGGTCTACTGCCTGCATGACACTC 600

Qy        2069 ACGATGCACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGG 2128
                |||||||||||||  |  |||||||||||||||||||||||  ||||||||||||||||
Db         601 ACGATGCACTCAACGTAGTGGTGCAGCTGGAGAAGCAGCTGCAGGGACAGCTGATCCAGG 660

Qy        2129 AGCCACGGGTCCTGCACTTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATG 2188
                |||||| ||| ||||||||||||||||||||||||||||||||||||| ||||||||||
Db         661 AGCCACTGGTACTGCACTTCAAGGACAGTTACCACAACCTGCGCCTATNCATCCACGATG 720

Qy        2189 TGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCTTT 2244
                ||||||||| ||    | |||||||||| ||||||||||||  ||||||| || |
Db         721 TGCCCAGCTNCCNTGTGGAGAGTAAGCTTCTTGTCAGCTACCCAGAGATCCNCTAT 776
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RESULT 12
BX348193/c
LOCUS       BX348193                796 bp    mRNA    linear   EST 08-APR-2004
DEFINITION  BX348193 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
            cDNA clone CS0DB008YE02 5-PRIME, mRNA sequence.
ACCESSION   BX348193
VERSION     BX348193.2  GI:46286231
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 796)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On May 5, 2003 this sequence version replaced gi:30367258.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            3239.r
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0BAF004ZD01_AF00293_1&c=3239.r
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FEATURES             Location/Qualifiers
     source          1. .796
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                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             26.2%;  Score 721.6;  DB 5;  Length 796;
  Best Local Similarity   96.4%;  Pred. No. 1.3e-141;
  Matches  758;  Conservative    0;  Mismatches   26;  Indels    2;  Gaps    2;

Qy       1679 GGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCTG 1738
              | |  |||  | | ||||||||||||||| |||||||||| |||||||||| | ||||||
Db        795 GTTGCCCCAAACCGGGCTGTCAGACCCTGTTGAGTCCCATGGTTAGCTGTGAA-CCCCTG 737

Qy       1739 GCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTG 1798
              ||||||||||||||| | |||||||||||| ||||||||||||||||||||||||||||||
Db        736 GCGTCCTGCTCACCGGCCCAGTCATCCTGGGTATGGACCACTGTGGGGAGCCCAGCCCTG 677

Qy       1799 ACAGCTGGAGCCTGCGCCTC-AAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTG 1857
              |||||||  |||||||||||| ||||| |||||||||||| |||||||||| |||| |||
Db        676 ACAGCTGAGGCCTGCGCCTCAAAAAAACAGTCGTGCGAGGACAGCTGGGAGTATGTCCTG 617

Qy       1858 CACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGC 1917
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 CACCTGGGCGAGNAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGC 557

Qy       1918 TACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCT 1977
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Db        556 TACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCT 497

Qy       1978 GCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTAC 2037
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Db        496 GCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTAC 437

Qy       2038 AACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTG 2097
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 AACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTG 377

Qy       2098 GAGAAGCAGCTGGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGACAGT 2157
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Db        376 GAGAAGCAGCTGGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGACAGT 317

Qy       2158 TACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTC 2217
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTC 257

Qy       2218 CTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTG 2277
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Db        256 CTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTG 197

Qy       2278 CACTGCACCTTCACCCTGGAGCGTGTCAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTG 2337
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Qy       2338 TGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAG 2397
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Db        136 TGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAG 77

Qy       2398 GACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTG 2457
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||   |
Db         76 GACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGNCCCTGGT 17

Qy       2458 GGCCCC 2463
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Db         16 GGGCCC 11
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RESULT 13
BI818609
LOCUS       BI818609                 818 bp    mRNA    linear   EST 04-OCT-2001
DEFINITION  603033362F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5174559 5',
            mRNA sequence.
ACCESSION   BI818609
VERSION     BI818609.1  GI:15929902
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 818)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11434 row: 1 column: 16
High quality sequence stop: 744.

FEATURES Location/Qualifiers
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/clone="IMAGE:5174559"
/lab_host="DH10B"
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/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 26.0%; Score 716.4; DB 4; Length 818;
Best Local Similarity 97.7%; Pred. No. 1.7e-140;
Matches 748; Conservative 0; Mismatches 16; Indels 2; Gaps 2;

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Qy         43 GCCATGGCCGTCCGGCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGG 102
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Db          1 GCCATGGCCGTCCGGCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGG 60

Qy        103 CTCCGCGGCTCGGGTGCCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAAC 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTCCGCGGCTCGGGTGCCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAAC 120

Qy        163 CCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAG 222
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Db        121 CCGGACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAG 180

Qy        223 CCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGG 282
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Db        181 CCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGG 240

Qy        283 GAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTG 342
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Db        241 GAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTG 300

Qy        343 CCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCGGGCTG 402
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        463 GCCTACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAG 522
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Qy        523 GTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCC 582
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Db        481 GTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCC 540

Qy        583 GAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATAC 642
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Qy        643 ATCACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTAC 702
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Db        601 ATCACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTAC 660

Qy        703 ACCTGCGTGGCCAAGAACATCGTGGCACGTC-GCCGCAGCGCCTCCGCTGCTGTCATCGT 761
              |||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||||
Db        661 ACCTGCGTGGCCAAGAACATCGTGGCACGTCAGCCGCAGGGCCTCCGCTGCTGTCATCGT 720

Qy        762 CTACGTGAACGGTGGGTGGTCGACG-TGGACCGAGTGGTCCGTCTG 806
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Db        721 CTACGTGGACGGCAGCTGGAGCCCGTTGGAGCCAGTGGTCGGGCTG 766
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RESULT 14
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LOCUS       BX364574                853 bp    mRNA    linear   EST 08-APR-2004
DEFINITION  BX364574 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DC023YB10 5-PRIME, mRNA sequence.
ACCESSION   BX364574
VERSION     BX364574.2  GI:46286957
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 853)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On May 5, 2003 this sequence version replaced gi:30368812.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            3529.f
            For more information about this cluster, see
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http://www.genoscope.cns.fr/cdna?s=CS1AC006ZF06QP1&c=3529.f.

FEATURES Location/Qualifiers.

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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 25.1%; Score 692; DB 5; Length 853;
Best Local Similarity 99.0%; Pred. No. 2.4e-135;
Matches 703; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

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Qy          1 CCGCGGGGCCCCGCGCCCGGCCCGCCCGCCTGCCCGCCCGCGGCCATGGCCGTCCGGCCC 60
              ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 CCGCRGGGCCCCGCGCCCGGCCCGCCCGCCTGCCCGCCCGCGGCCATGGCCGTCCGGCCC 204

Qy         61 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 264

Qy        121 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC 180
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Db        265 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCYAACCCGGACCTGCTTCCCCAC 324

Qy        181 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 240
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Db        325 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 384

Qy        241 AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 300
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Db        385 AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 444

Qy        301 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGC 360
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Qy        361 ATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCGGGCTGGAGGAATACTGGTGCCAG 420
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Db        504 ATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCGGGCTGGAGGAATACTGGTGCCAG 563

Qy        421 TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 480
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Db        624 TATTTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 683

Qy        541 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600
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Db        744 AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 803

Qy        661 CTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGT 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        804 CTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGT 853


RESULT 15
AY411748
LOCUS       AY411748                2532 bp    DNA     linear   GSS 12-DEC-2003
DEFINITION  Pan troglodytes HCM4327 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY411748
VERSION     AY411748.1  GI:39767716
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 2532)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 2532)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             24.6%;  Score 678.2;  DB 9;  Length 2532;
  Best Local Similarity   54.4%;  Pred. No. 2.2e-132;
  Matches 1370;  Conservative    0;  Mismatches 1021;  Indels  129;  Gaps    9;

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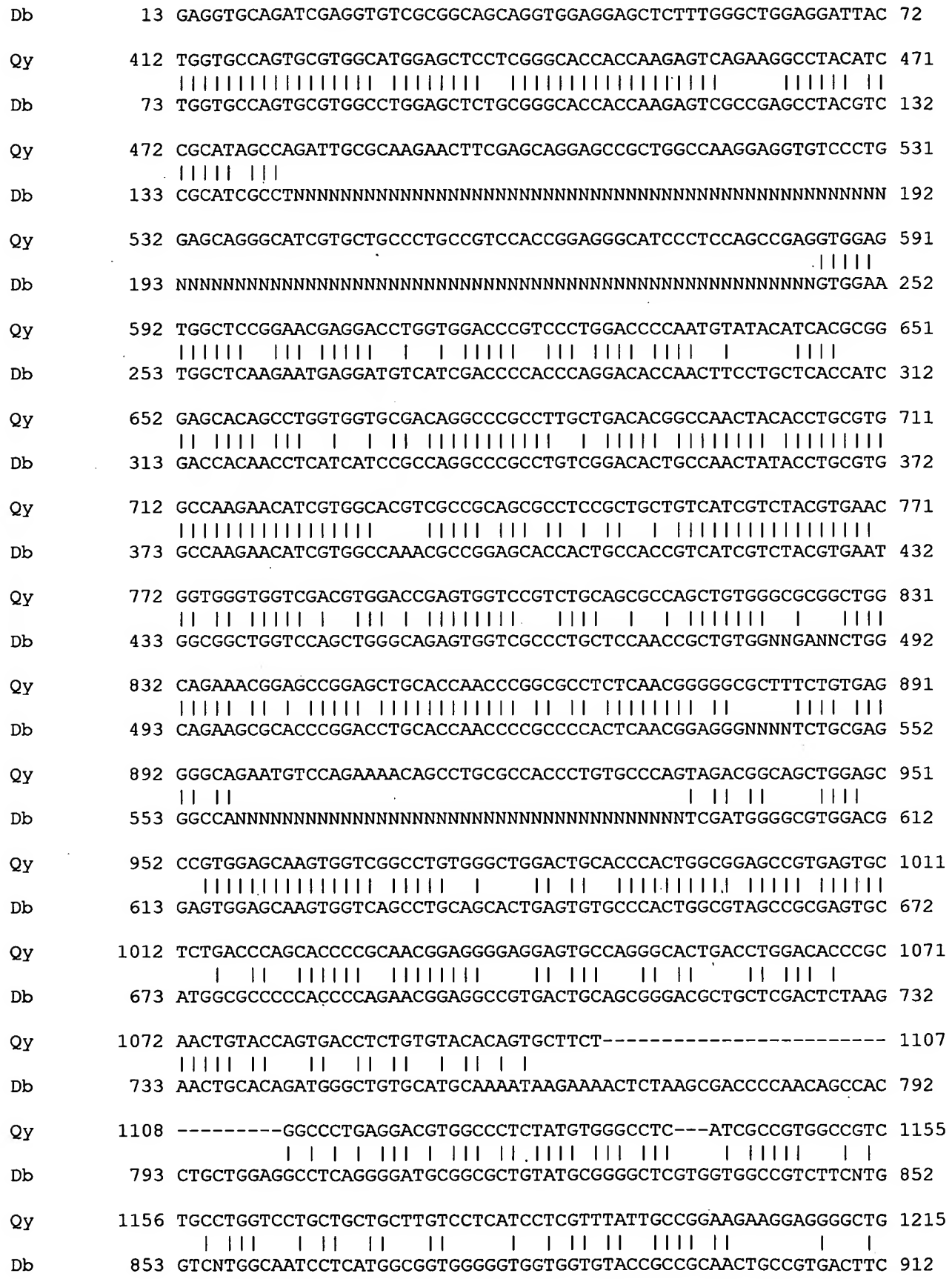

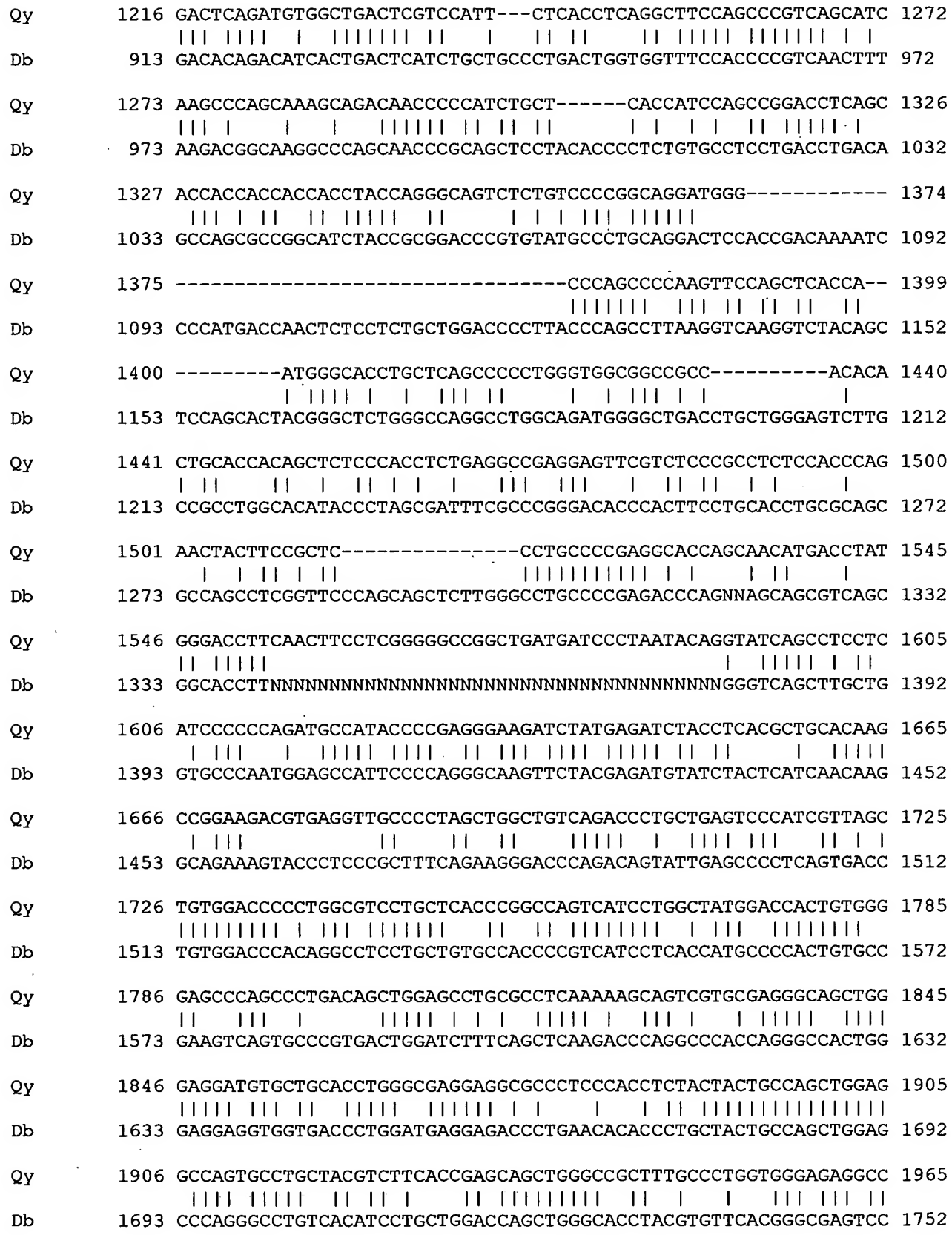

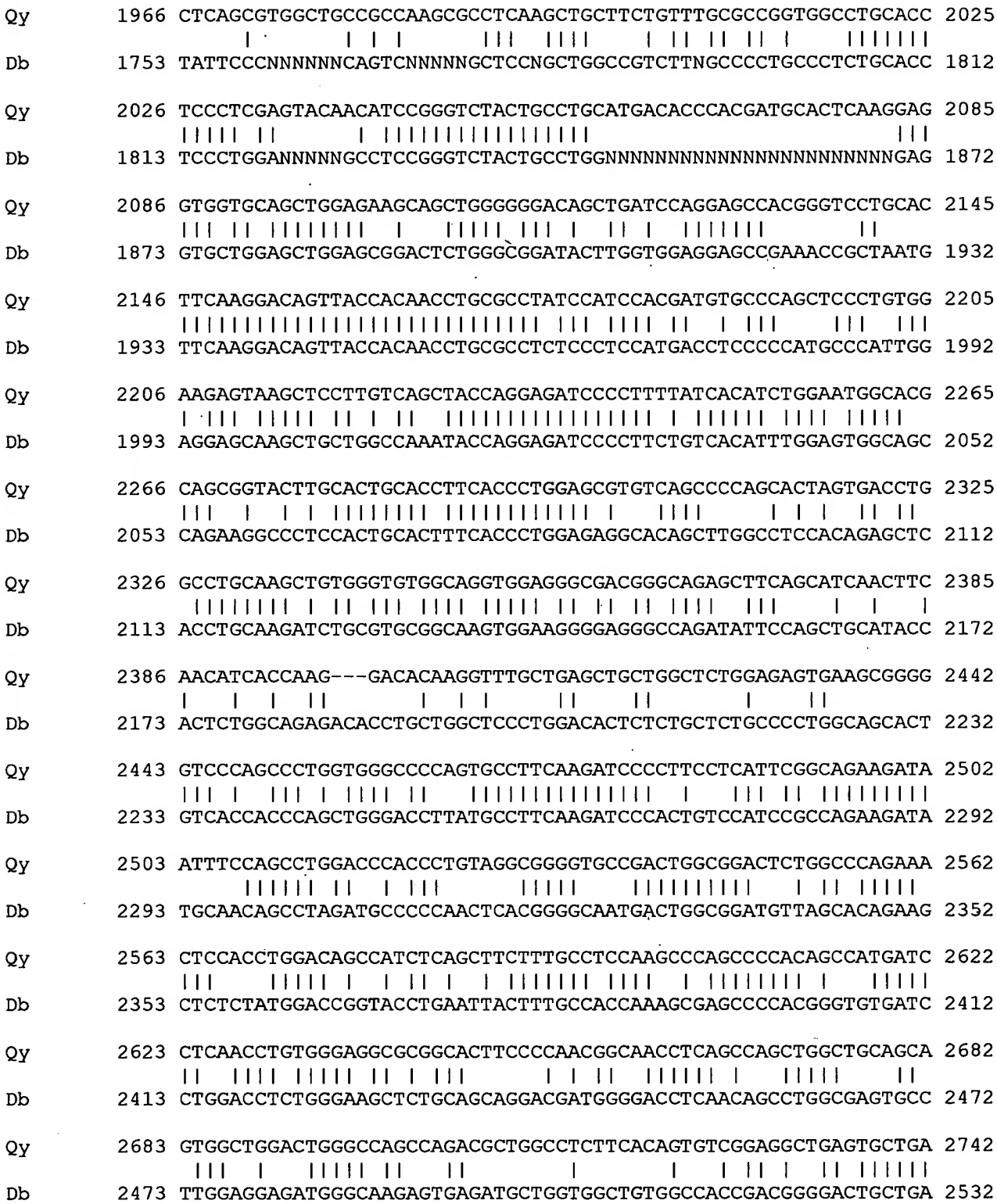

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Job time : 8663.89 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 5, 2005, 15:11:26 ; Search time 11689.8 Seconds
(without alignments)
11407.261 Million cell updates/sec

Title: US-10-624-932-1
Perfect score: 2752
Sequence: 1 ccgcggggccccgcgcccgg.....tgagtgctgaggccggccag 2752

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2752	100.0	2752	6	AX449572	AX449572 Sequence
2	2687.4	97.7	2697	6	AX451652	AX451652 Sequence
3	2676.4	97.3	2881	6	AX527916	AX527916 Sequence

4	2435.4	88.5	2784	6	CQ730306	CQ730306 Sequence
5	2356	85.6	3580	6	AX367094	AX367094 Sequence
6	2323.2	84.4	3992	10	MMU487852	AJ487852 Mus muscu
7	2259	82.1	3014	6	BD057524	BD057524 Netrin re
8	2252.2	81.8	2697	6	AX268596	AX268596 Sequence
9	2252.2	81.8	2697	10	RNU87305	U87305 Rattus norv
10	1983.6	72.1	3844	10	BC058084	BC058084 Mus muscu
11	1635.4	59.4	2688	9	BC009333	BC009333 Homo sapi
12	1562.4	56.8	1787	6	BD057525	BD057525 Netrin re
13	1304.2	47.4	9700	6	AX054976	AX054976 Sequence
14	992	36.0	9299	10	MMU72634	U72634 Mus musculu
15	991	36.0	2962	5	AY187310	AY187310 Gallus ga
16	986	35.8	9328	10	AB118026	AB118026 Rattus no
17	970	35.2	3646	6	CQ881060	CQ881060 Sequence
18	970	35.2	3646	9	AF055634	AF055634 Homo sapi
19	943.8	34.3	3770	9	AY126437	AY126437 Homo sapi
20	936.2	34.0	2860	6	AX686445	AX686445 Sequence
21	936.2	34.0	2860	6	AX686447	AX686447 Sequence
22	913.8	33.2	3672	10	BC048162	BC048162 Mus muscu
23	913.8	33.2	3672	10	BC057560	BC057560 Mus muscu
24	913.6	33.2	2895	6	AX512281	AX512281 Sequence
25	905.6	32.9	3933	6	CQ850929	CQ850929 Sequence
26	905.6	32.9	3933	9	AK128132	AK128132 Homo sapi
27	905.6	32.9	3935	9	AB096256	AB096256 Homo sapi
28	904.2	32.9	2986	6	CQ881052	CQ881052 Sequence
29	902.4	32.8	3884	6	AR528525	AR528525 Sequence
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31	902.4	32.8	3884	9	AY358351	AY358351 Homo sapi
32	893.8	32.5	2995	6	AX497288	AX497288 Sequence
33	892	32.4	4294	10	AK122575	AK122575 Mus muscu
34	875.6	31.8	3788	10	MMU487853	AJ487853 Mus muscu
35	852.4	31.0	2838	10	RNU87306	U87306 Rattus norv
36	843.6	30.7	2625	6	CQ721377	CQ721377 Sequence
37	841.4	30.6	2831	6	BD057526	BD057526 Netrin re
38	764.8	27.8	813	6	AX054892	AX054892 Sequence
39	753.6	27.4	2230	6	CQ845766	CQ845766 Sequence
40	753.6	27.4	2230	9	AK131380	AK131380 Homo sapi
41	751.4	27.3	4330	5	AY744919	AY744919 Petromyzo
42	717.2	26.1	2832	5	AY099459	AY099459 Xenopus l
43	668.4	24.3	2612	6	CQ881064	CQ881064 Sequence
44	623.2	22.6	2661	6	AX800717	AX800717 Sequence
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ALIGNMENTS

RESULT 1
AX449572
LOCUS AX449572 2752 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 1 from Patent WO0210216.
ACCESSION AX449572
VERSION AX449572.1 GI:21698195
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Padigaru,M., Mezes,P., Mishra,V., Burgess,C., Casman,S., Grosse,W.M., Alsobrook,J.P., Lepley,D.M., Gerlach,V.L., Macdougall,J.R. and Smithson,G.
TITLE Proteins and nucleic acids encoding same
JOURNAL Patent: WO 0210216-A 1 07-FEB-2002; Curagen Corporation (US)

FEATURES Location/Qualifiers
source 1. .2752
/organism="Homo sapiens"
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/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 2752; DB 6; Length 2752;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CCGCGGGGCCCCGCGCCCGGCCCGCCCGCCTGCCCGCCCGCGGCCATGGCCGTCCGGCCC 60
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Qy         61 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 120
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Qy        121 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC 180
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Qy        181 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 240
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Qy        781 TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG 840
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Qy        961 AAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCA 1020
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Qy       1441 CTGCACCACAGCTCTCCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAG 1500
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Qy       2281 TGCACCTTCACCCTGGAGCGTGTCAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGG 2340
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Qy       2701 CCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGAGGCCGGCCAG 2752
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RESULT 2
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LOCUS       AX451652                2697 bp    DNA     linear   PAT 03-JUL-2002
DEFINITION  Sequence 1 from Patent WO0233080.
ACCESSION   AX451652
VERSION     AX451652.1  GI:21698587
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Koehler,R.H.
  TITLE     Regulation of human netrin binding membrane receptor unc5h-1
  JOURNAL   Patent: WO 0233080-A 1 25-APR-2002;
            Bayer Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
ORIGIN
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Query Match 97.7%; Score 2687.4; DB 6; Length 2697;

Best Local Similarity 99.8%; Pred. No. 0;
Matches 2691; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy       106 CGCGGCTCGGGTGCCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCG 165
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Db       721 GTGAACGGTGGGTGGTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGC 780

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Qy       1006 GAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGAC 1065
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Qy       1246 ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTC 1305
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Qy       1306 ACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGG 1365
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Qy       1366 CAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGT 1425
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Qy       1486 CGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTAT 1545
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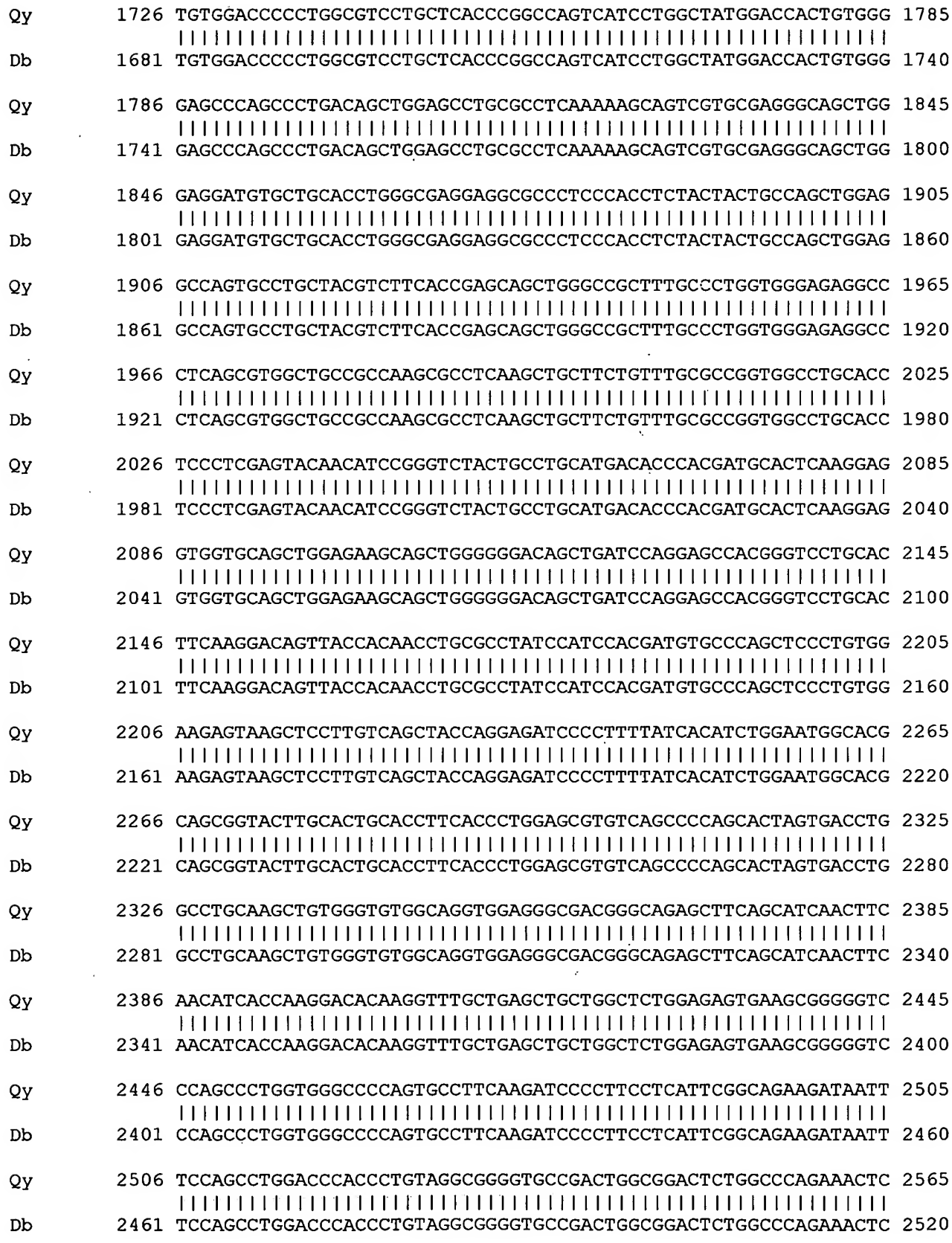
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Qy 1966 CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC 2025
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Qy 2026 TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG 2085
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Qy 2326 GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTC 2385
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Qy       2626 AACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTG 2685
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Qy       2686 GCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGA 2742
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Db       2641 GCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGA 2697


RESULT 3
AX527916
LOCUS       AX527916                2881 bp    DNA     linear   PAT 21-NOV-2002
DEFINITION  Sequence 1 from Patent WO0229038.
ACCESSION   AX527916
VERSION     AX527916.1  GI:25172359
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Herrmann,J.L., Rastelli,L. and Shimkets,R.A.
  TITLE     Novel proteins and nucleic acids encoding same and antibodies
            directed against these proteins
  JOURNAL   Patent: WO 0229038-A 1 11-APR-2002;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
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  Best Local Similarity   98.9%;  Pred. No. 0;
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Qy         61 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 120
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Qy        121 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC 180
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Qy        181 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 240
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Db        222 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 281
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Qy        241 AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 300
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Db        282 AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 341

Qy        301 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGC 360
              |||||||||||||||||||||||||||||||||||   ||| ||||||||||||||||
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Qy        361 ATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCGGGCTGGAGGAATACTGGTGCCAG 420
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Qy        421 TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 480
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Qy        541 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600
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Qy        601 AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 660
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Db        642 AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 701

Qy        661 CTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAAC 720
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Qy        721 ATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGG 780
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Db        762 ATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGG 821

Qy        781 TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG 840
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Db        822 TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG 881

Qy        841 AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT 900
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Qy        901 GTCCAGAA---AACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGG 957
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Db        942 GTCCATGACCGCACCGTCTCCTCTCTGCTTGTCTCTGTGGACGGCAGCTGGAGCCCGTGG 1001

Qy        958 AGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGAC 1017
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Qy       1018 CCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGT 1077
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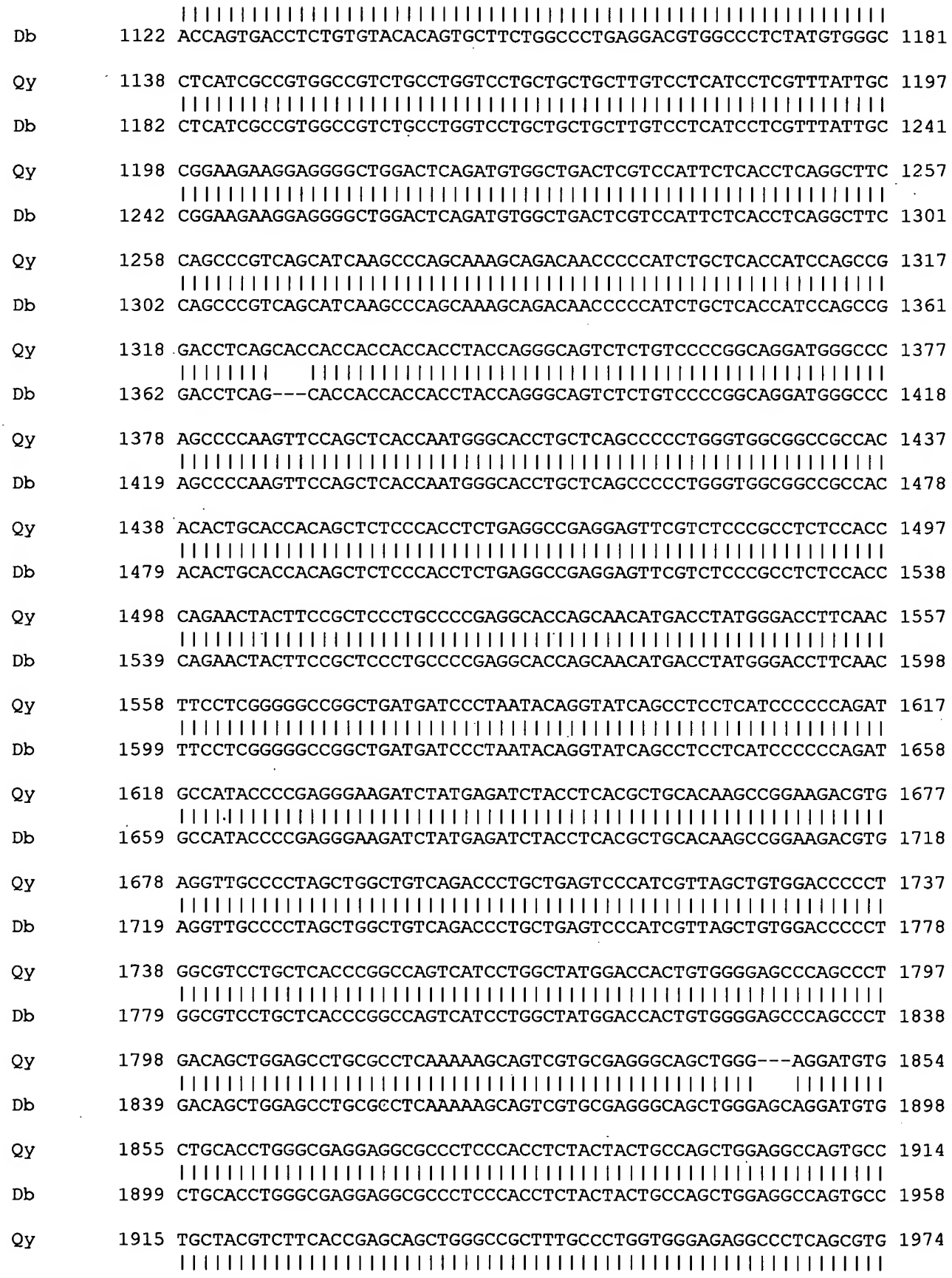

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Qy       2035 TACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAG 2094
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Qy       2155 AGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAG 2214
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Qy       2215 CTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTAC 2274
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Qy       2395 AAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTG 2454
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Qy       2455 GTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTG 2514
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RESULT 4
CQ730306

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LOCUS       CQ730306                2784 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 16240 from Patent WO02068579.
ACCESSION   CQ730306
VERSION     CQ730306.1  GI:42303801
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 16240 06-SEP-2002;
            PE Corporation (NY) (US)
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ORIGIN

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  Best Local Similarity   93.5%;  Pred. No. 0;
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Qy        106 CGCGGCTCGGGTGCCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCG 165
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Db         61 CGCGGCTCGGGTGCCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCG 120

Qy        166 GACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCA 225
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Db        121 GACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCA 180

Qy        226 GTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAG 285
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Qy        286 TGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCC 345
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Qy        346 ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCGGGCTGGAG 405
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Qy        406 GAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC 465
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Db        361 GAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC 420

Qy        466 TACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG 525
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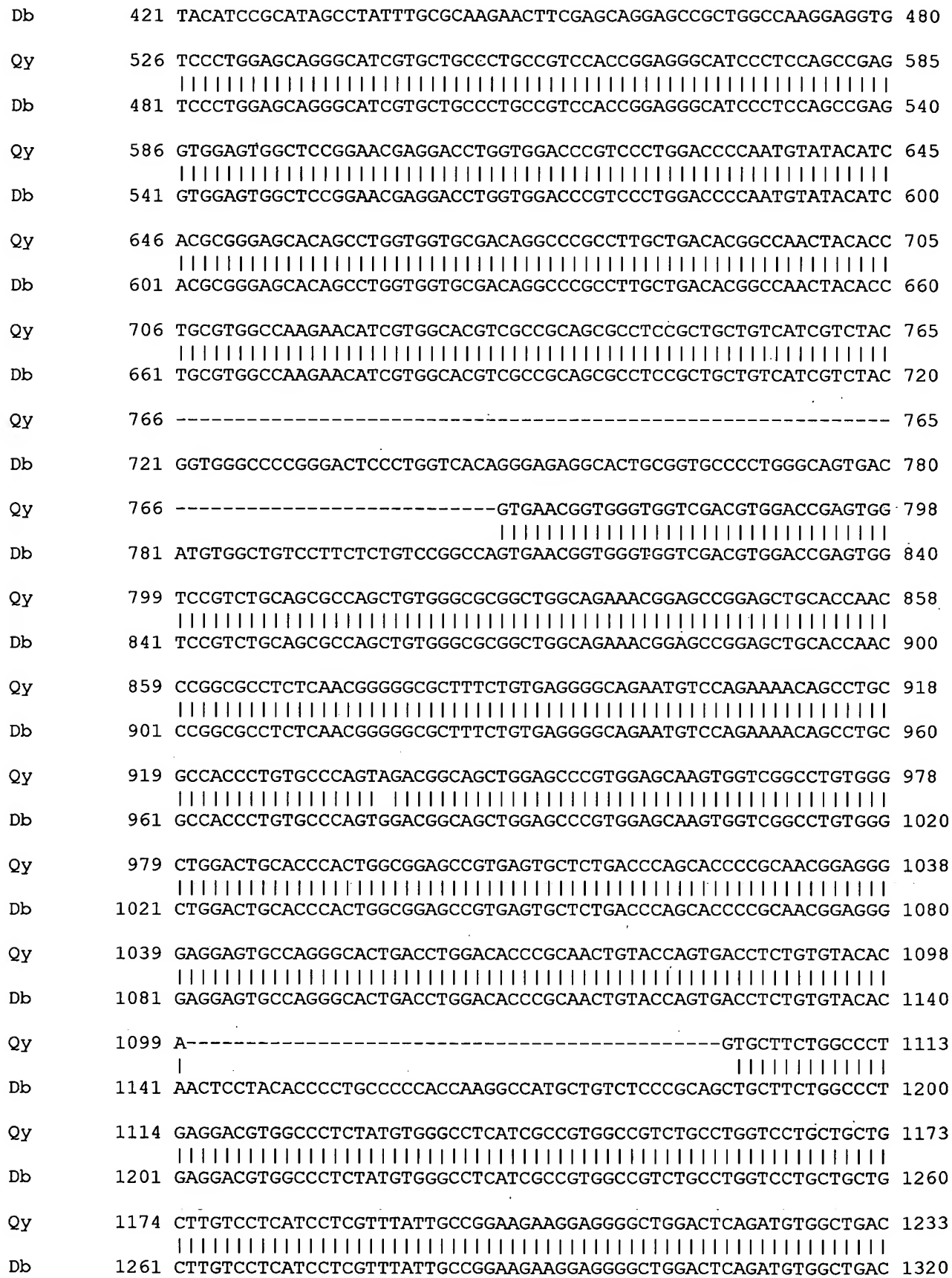
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Qy 586 GTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATC 645
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Qy 919 GCCACCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGG 978
Db 961 GCCACCCTGTGCCCAGTGGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGG 1020
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Db       1321 TCGTCCATTCTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAAC 1380

Qy       1294 CCCCATCTGCTCACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGT 1353
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Qy       1354 CTCTGTCCCCGGCAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTC 1413
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Qy       1414 AGCCCCCTGGGTGGCGGCCGCCACACACTGCACCACAGCTCTCCCACCTCTGAGGCCGAG 1473
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Qy       2134 CGGGTCCTGCACTTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCC 2193
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Qy       2674 GCTGCAGCAGTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTCGGAGGCT 2733
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RESULT 5
AX367094
LOCUS AX367094 3580 bp DNA linear PAT 16-FEB-2002
DEFINITION Sequence 13 from Patent WO0198354.
ACCESSION AX367094
VERSION AX367094.1 GI:18855296
KEYWORDS .
SOURCE Homo sapiens (human)

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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Griffin,J.A., Kallick,D.A., Tribouley,C.M., Yue,H., Nguyen,D.B.,
            Tang,Y.T., Lal,P., Policky,J.L., Azimzai,Y., Lu,D.A., Graul,R.,
            Yao,M.G., Burford,N., Hafalia,A.J., Baughn,M.R., Bandman,O.,
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            Sanjanwala,M.S.
  TITLE     Receptors
  JOURNAL   Patent: WO 0198354-A 13 27-DEC-2001;
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

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Qy        103 CTCCGCGGCTCGGGTGCCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAAC 162
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Qy        343 CCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCGGGCTG 402
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Db        301 CCCACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCGGGCTG 360

Qy        403 GAGGAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAG 462
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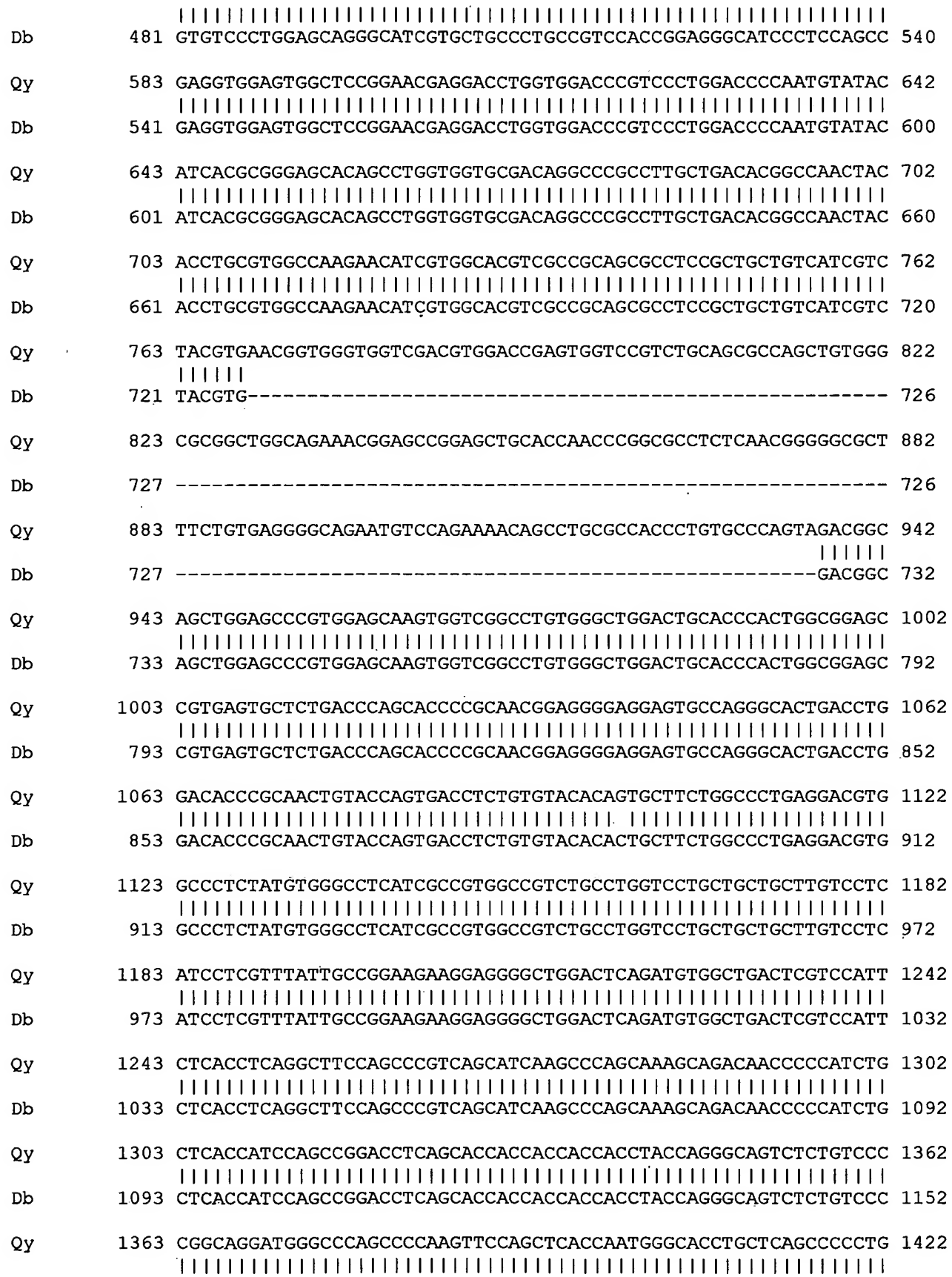

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Qy       1663 AAGCCGGAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTT 1722
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Qy       2143 CACTTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTG 2202
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RESULT 6
MMU487852
LOCUS       MMU487852               3992 bp    mRNA    linear   ROD 24-SEP-2002
DEFINITION  Mus musculus mRNA for netrin receptor Unc5h1 (Unc5h1 gene).
ACCESSION   AJ487852
VERSION     AJ487852.1  GI:22035783
KEYWORDS    netrin receptor Unc5h1; Unc5h1 gene.
SOURCE      Mus musculus (house mouse)
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REFERENCE   1
  AUTHORS   Engelkamp,D.
  TITLE     Cloning of three mouse Unc5 genes and their expression patterns at
            mid-gestation
  JOURNAL   Mech. Dev. 118 (1-2), 191-197 (2002)
  MEDLINE   22239710
   PUBMED   12351186
REFERENCE   2  (bases 1 to 3992)
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  AUTHORS   Engelkamp,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-MAY-2002) Neuroanatomy, Max Planck Institute for
            Brain Research, Deutschordenstrasse 46, Frankfurt 60528, GERMANY
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ORIGIN

  Query Match             84.4%;  Score 2323.2;  DB 10;  Length 3992;
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Db        187 CCGCCCGCGGGGCCCCTAGTCCAGCCCGCTCGTCCGCCCGCGGCCATGGCCGTCCGGCCC 246

Qy         61 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 120
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Qy        121 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC 180
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Qy        181 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 240
              |||||||| ||||| ||||| |||||||| |||||||||||||| |||||||| ||||||
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Qy       241 AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 300
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Db       427 AAGGCTGTGCCCGCCACCCAGATCTTCTTCAAGTGCAACGGGGAATGGGTTCGCCAGGTC 486

Qy       301 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGC 360
            || ||||| ||||| |||||||| ||||| ||||| ||  |||| ||||||||||||||
Db       487 GATCACGTCATCGAACGCAGCACTGACGGCAGCAGCGGATTGCCAACCATGGAGGTCCGG 546

Qy       361 ATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCGGGCTGGAGGAATACTGGTGCCAG 420
            || || || |||||||||||||||||||| ||||| |||||||||| ||||||||||||
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Qy       421 TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 480
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Qy       481 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 540
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Db       667 TATTTGCGCAAGAACTTTGAGCAGGAGCCGCTGGCCAAGGAAGTGTCACTGGAGCAAGGC 726

Qy       541 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600
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Qy       601 AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 660
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Db      1087 GTCCAGAAAACAGCCTGCGCCACTCTGTGCCCAGTGGATGGGAGCTGGAGCCCATGGAGT 1146

Qy       961 AAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCA 1020
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Db      1147 AAGTGGTCAGCCTGCGGGCTTGACTGCACCCACTGGCGGAGCCGGGAGTGCTCCGACCCA 1206

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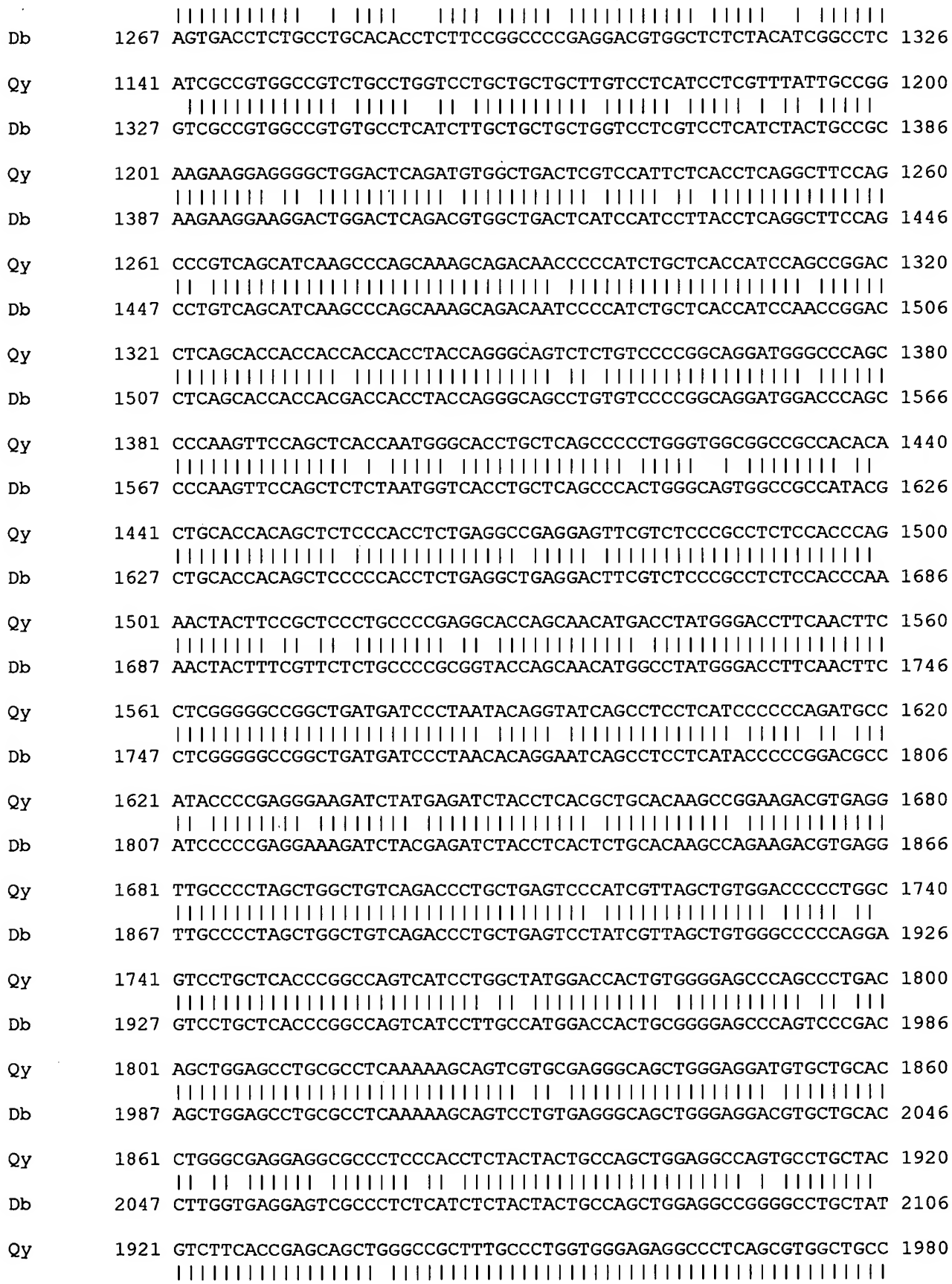

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Db       2527 GTGTGGCAGGTGGAGGGAGATGGACAGAGCTTCAACATCAACTTTAACATCACTAAGGAC 2586

Qy       2401 ACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGC 2460
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Db       2587 ACGAGGTTTGCTGAAATGCTGGCTCTGGAGAGTGAAGGGGGGGTCCCAGCCCTGGTGGGC 2646

Qy       2461 CCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGACCCA 2520
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Qy       2581 CTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCG 2640
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Qy       2641 CGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAG 2700
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Db       2827 CGGCACTTCCCCAACGGCAACCTCGGCCAGCTGGCCGCAGCTGTGGCCGGACTGGGCCAG 2886

Qy       2701 CCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGAGGCCGGCCAG 2752
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RESULT 7
BD057524

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LOCUS       BD057524                3014 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Netrin receptors.
ACCESSION   BD057524
VERSION     BD057524.1  GI:22603130
KEYWORDS    JP 2001505062-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 3014)
  AUTHORS   Lavigne,M.T., Leonardo,D.E., Hinck,L., Masu,M. and Masu,K.K.
  TITLE     Netrin receptors
  JOURNAL   Patent: JP 2001505062-A 1 17-APR-2001;
            THE REGENTS OF THE UNIV OF CALIFORNIA
COMMENT     PN   JP 2001505062-A/1
            PD   17-APR-2001
            PF   19-FEB-1998 JP 1998536840
            PR   19-FEB-1997 US    08/808982
            PI   MARC TESSIER LAVIGNE,DAVID E LEONARDO,LINDSAY HINCK,MASAYUKI
            PI   MASU,
            PI   KAZUKO KEINO MASU
            PC   C07K1/00,C07K14/00,C07K17/00,C07H21/02,C07H21/04,G01N33/53 CC
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            FH   Key             Location/Qualifiers.
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ORIGIN

  Query Match             82.1%;  Score 2259;  DB 6;  Length 3014;
  Best Local Similarity   89.7%;  Pred. No. 0;
  Matches 2427;  Conservative    0;  Mismatches  280;  Indels    0;  Gaps    0;

Qy         46 ATGGCCGTCCGGCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTC 105
              ||||||||||||||||||||||||||| |||||||||||||||||||||| |||||
Db          1 ATGGCCGTCCGGCCCGGCCTGTGGCCAGTGCTCCTGGGCATAGTCCTCGCCGCCTGGCTT 60

Qy        106 CGCGGCTCGGGTGCCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCG 165
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Qy        166 GACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCA 225
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Db        121 GACCTGCTGCCCCACTTCCTGGTAGAGCCTGAGGACGTGTACATTGTCAAGAACAAGCCG 180

Qy        226 GTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAG 285
              ||| || | |||||||||||| ||||| ||||| ||||||||||||||||||| |||||
Db        181 GTGTTGTTGGTGTGCAAGGCTGTGCCTGCCACCCAGATCTTCTTCAAGTGCAATGGGGAA 240

Qy        286 TGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCC 345
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Db        241 TGGGTCCGCCAGGTCGATCACGTAATTGAACGCAGCACCGACAGCAGCAGCGGATTGCCA 300

Qy        346 ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCGGGCTGGAG 405
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Db        301 ACCATGGAGGTCCGTATCAACGTATCGAGGCAGCAGGTAGAGAAAGTGTTTGGGCTGGAG 360

Qy        406 GAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC 465
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Qy        586 GTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATC 645
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Qy        646 ACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACC 705
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Qy        706 TGCGTGGCCAAGAACATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTCATCGTCTAC 765
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Qy        766 GTGAACGGTGGGTGGTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGC 825
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Qy        826 GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTC 885
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Db        781 GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCACCTCTCAACGGGGGCGCCTTC 840

Qy        886 TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGC 945
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Db        841 TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACTCTGTGCCCAGTGGATGGGAGC 900

Qy        946 TGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGT 1005
              |||||  ||||||| |||||||| |||||||||| ||||||||||||||||||||||
Db        901 TGGAGTTCGTGGAGTAAGTGGTCAGCCTGTGGGCTTGACTGCACCCACTGGCGGAGCCGC 960

Qy       1006 GAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGAC 1065
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Db        961 GAGTGCTCTGACCCAGCACCCCGCAATGGAGGTGAGGAGTGTCGGGGTGCTGACCTGGAC 1020

Qy       1066 ACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCC 1125
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Qy       1126 CTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCTCATC 1185
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Qy       1186 CTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTC 1245
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Qy       1246 ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTC 1305
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Db       1261 ACCATCCAGCCAGACCTCAGCACCACCACTACCACCTACCAGGGCAGTCTATGTTCGAGG 1320

Qy       1366 CAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGT 1425
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Qy       1426 GGCGGCCGCCACACACTGCACCACAGCTCTCCCACCTCTGAGGCCGAGGAGTTCGTCTCC 1485
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Qy       1486 CGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTAT 1545
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Db       1501 GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACGGGGATCAGCCTCCTC 1560

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Qy       1666 CCGGAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGC 1725
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Qy       1726 TGTGGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGG 1785
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Qy       2026 TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG 2085
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Qy       2086 GTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCAC 2145
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Db       2161 AAGAGCAAGCTACTTGTCAGCTACCAGGAGATCCCTTTTTACCACATCTGGAACGGCACC 2220

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Db       2221 CAGCAGTATCTGCACTGCACCTTCACCCTGGAGCGCATCAACGCCAGCACCAGCGACCTG 2280

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Db       2281 GCCTGCAAGGTGTGGGTGTGGCAGGTGGAGGGAGATGGGCAGAGCTTCAACATCAACTTC 2340

Qy       2386 AACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTC 2445
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Qy       2446 CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATT 2505
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Db       2521 CACCTGGACAGCCATCTTAGCTTCTTTGCCTCCAAGCCCAGCCCTACAGCCATGATCCTC 2580

Qy       2626 AACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTG 2685
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Qy       2746 CGGCCAG 2752
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Db       2701 CAGCCAG 2707
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RESULT 8
AX268596
LOCUS       AX268596                2697 bp    DNA     linear   PAT 29-OCT-2001
DEFINITION  Sequence 15 from Patent WO0175440.
ACCESSION   AX268596
VERSION     AX268596.1  GI:16541710
KEYWORDS    .
SOURCE      Rattus sp.
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  ORGANISM  Rattus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1
  AUTHORS   Cochran,S.W., Paterson,G.Y., Ohashi,Y.W., Morris,B.Y. and
            Pratt,J.Y.
  TITLE     Schizophrenia related genes
  JOURNAL   Patent: WO 0175440-A 15 11-OCT-2001;
            WELFIDE CORPORATION (JP)
FEATURES             Location/Qualifiers
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ORIGIN

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Qy        406 GAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC 465
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Db        421 TACATCCGGATTGCCTATTTGCGCAAGAACTTTGAGCAGGAGCCACTGGCCAAGGAAGTG 480

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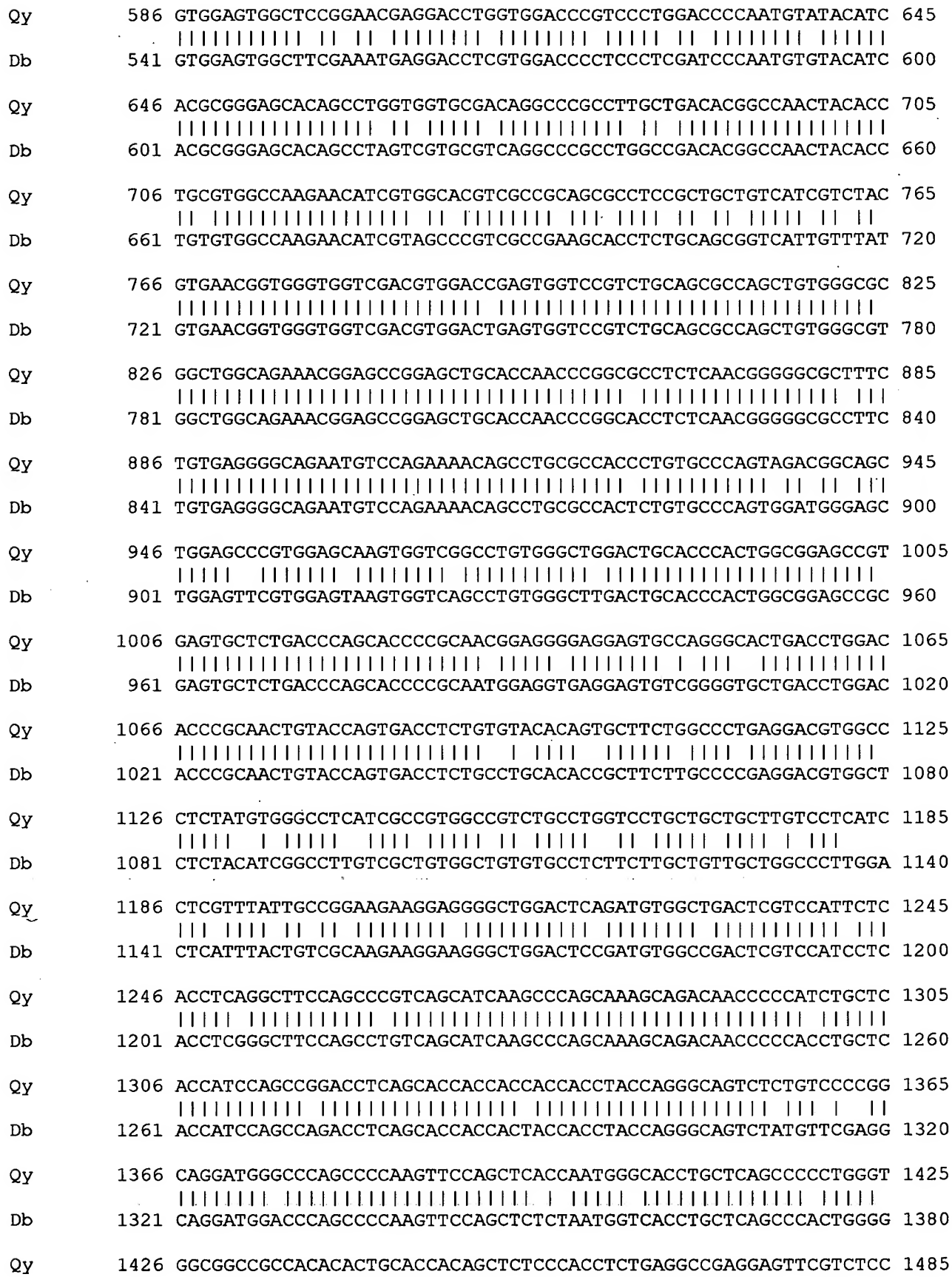

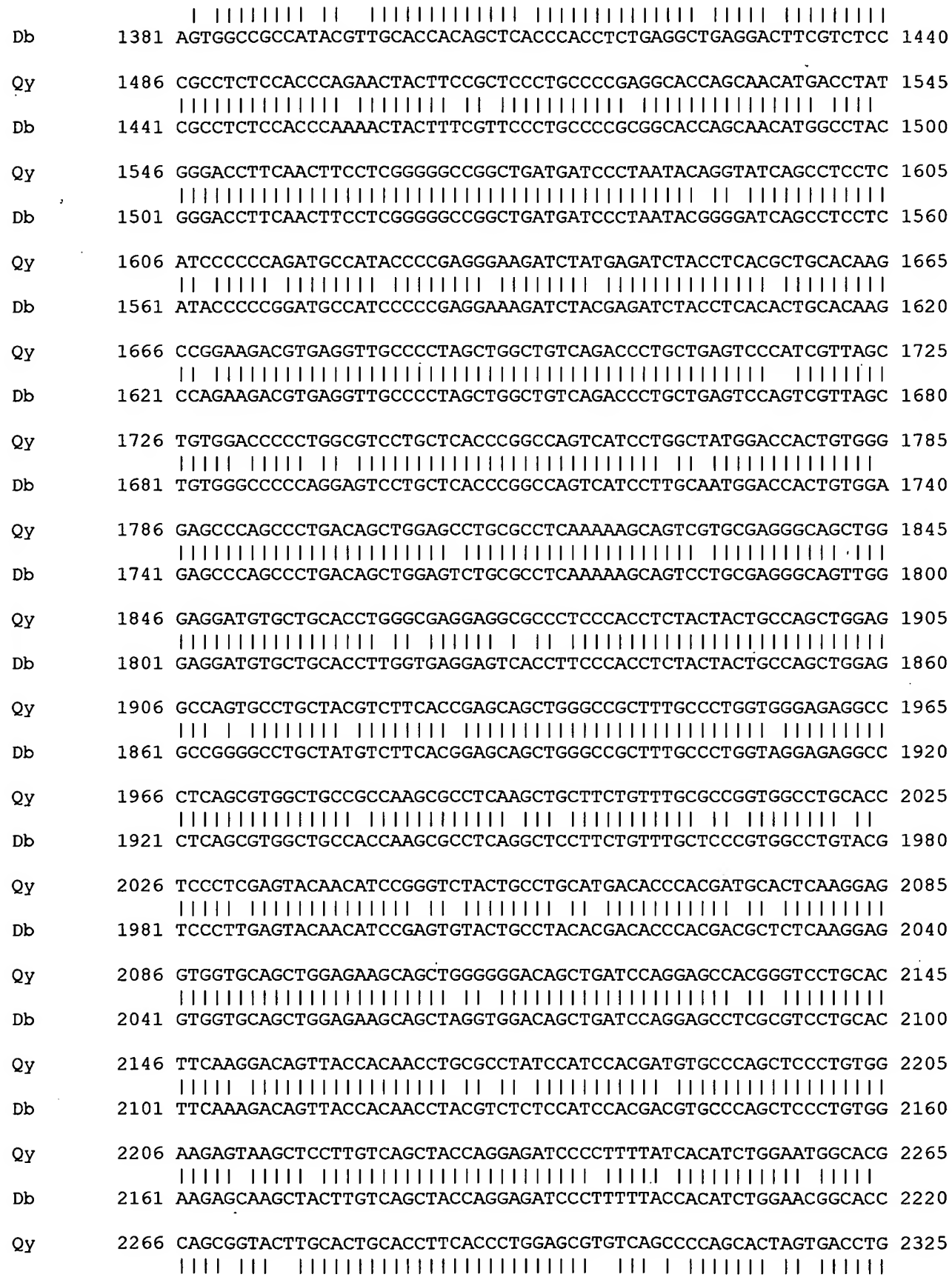

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RESULT 9
RNU87305
LOCUS       RNU87305                2697 bp    mRNA    linear   ROD 15-MAY-1997
DEFINITION  Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds.
ACCESSION   U87305
VERSION     U87305.1  GI:2055391
KEYWORDS    .
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 2697)
  AUTHORS   Leonardo,E.D., Hinck,L., Masu,M., Keino-Masu,K., Ackerman,S.L. and
            Tessier-Lavigne,M.
  TITLE     Vertebrate homologues of C. elegans UNC-5 are candidate netrin
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  JOURNAL   Nature 386 (6627), 833-838 (1997)
  MEDLINE   97271897
   PUBMED   9126742
REFERENCE   2  (bases 1 to 2697)
  AUTHORS   Leonardo,E.D., Hinck,L., Masu,M., Keino-Masu,K. and
            Tessier-Lavigne,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JAN-1997) Anatomy, UCSF, 513 Parnassus, San
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Qy        106 CGCGGCTCGGGTGCCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCG 165
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Qy        166 GACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCA 225
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Qy        286 TGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCC 345
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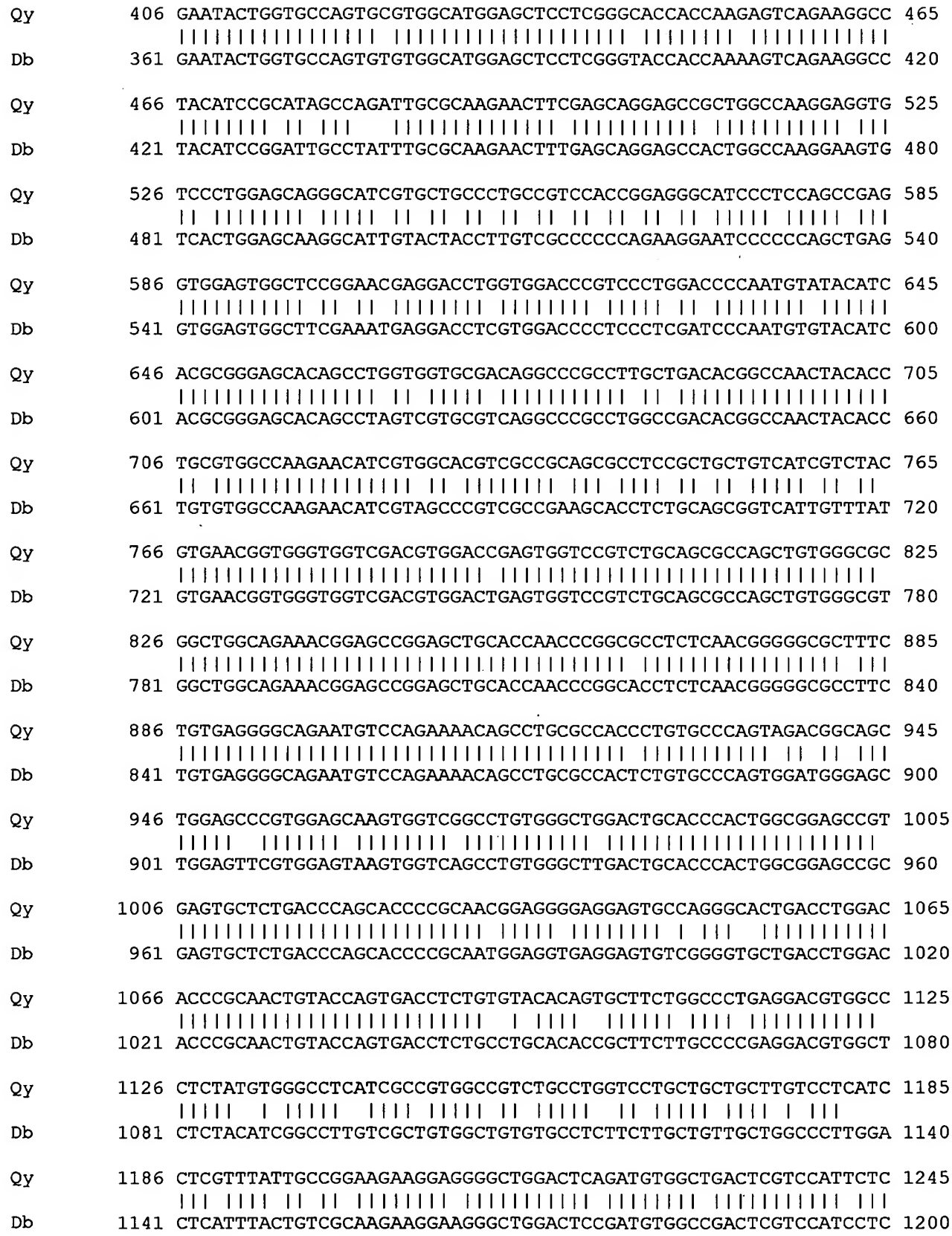

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Qy       1306 ACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGG 1365
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Qy       1486 CGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTAT 1545
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Qy       1666 CCGGAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGC 1725
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Qy       1906 GCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCC 1965
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Qy       1966 CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC 2025
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Db        2641 GCCGGACTGGGCCAACCAGATGCTGGCCTCTTCACGGTGTCGGAGGCCGAGTGTTGA 2697
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RESULT 10
BC058084
LOCUS       BC058084                3844 bp    mRNA    linear   ROD 21-OCT-2003
DEFINITION  Mus musculus unc-5 homolog A (C. elegans), mRNA (cDNA clone
            MGC:66671 IMAGE:6813463), complete cds.
ACCESSION   BC058084
VERSION     BC058084.1  GI:34784158
KEYWORDS    MGC.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 3844)
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AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257

PUBMED 12477932

REFERENCE 2 (bases 1 to 3844)

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (08-SEP-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov

COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 126 Row: b Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23346570.

FEATURES Location/Qualifiers

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Matches 2320; Conservative 0; Mismatches 264; Indels 168; Gaps 1;

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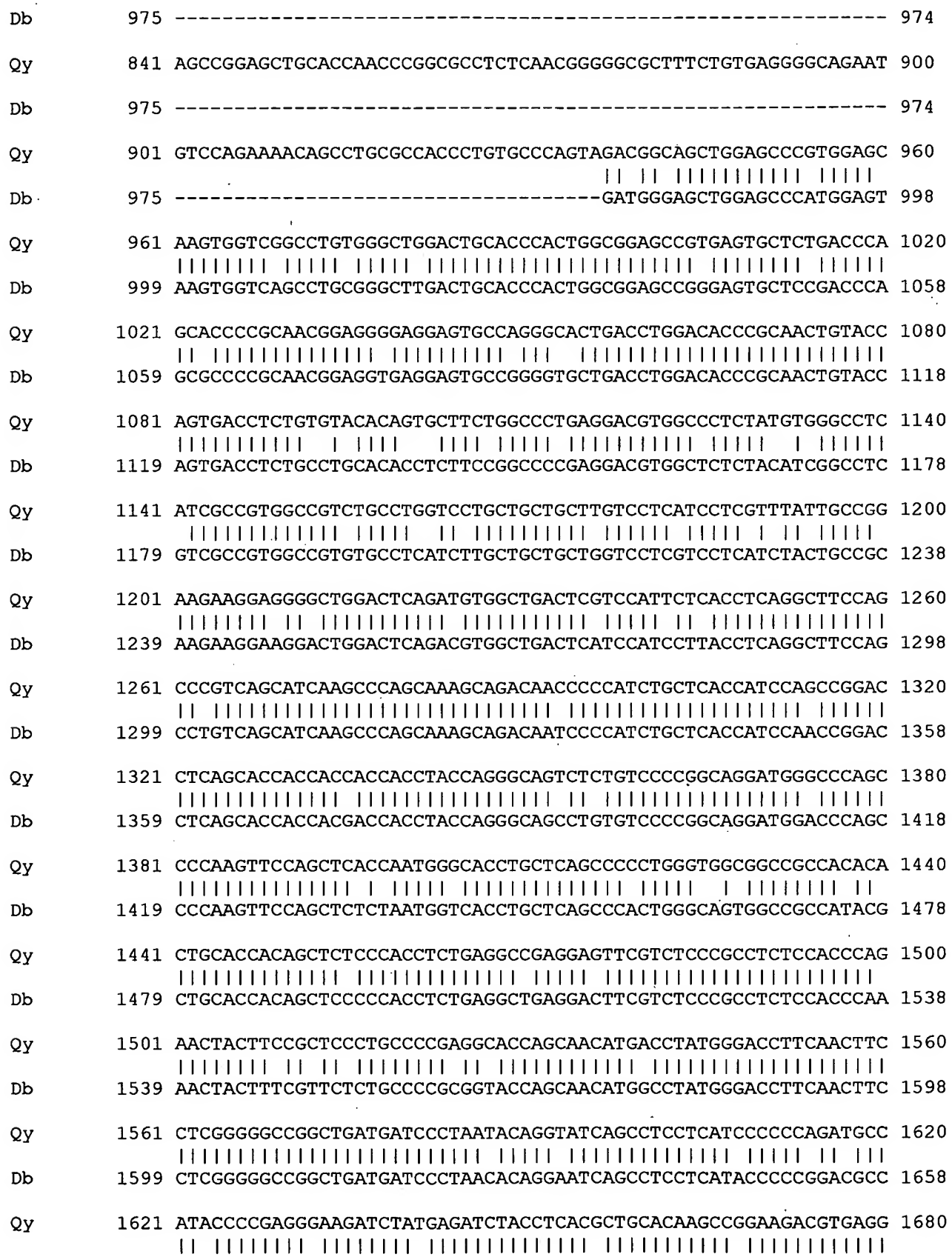

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RESULT 11
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DEFINITION Homo sapiens unc-5 homolog A (C. elegans), mRNA (cDNA clone IMAGE:4126760), partial cds.
ACCESSION BC009333
VERSION BC009333.2 GI:40226527
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2688)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCE 2 (bases 1 to 2688)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov

COMMENT On Dec 19, 2003 this sequence version replaced gi:14424611.
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 26 Row: g Column: 22.

FEATURES Location/Qualifiers

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ORIGIN

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Qy       1656 GCTGCACAAGCCGGAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCC 1715
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCTGCACAAGCCGGAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCC 600

Qy       1716 CATCGTTAGCTGTGGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGA 1775
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Db        601 CATCGTTAGCTGTGGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGA 660

Qy       1776 CCACTGTGGGGAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGA 1835
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCACTGTGGGGAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGA 720

Qy       1836 GGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTG 1895
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Db        721 GGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTG 780

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Db        781 CCAGCTGGAGGCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGT 840

Qy       1956 GGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGT 2015
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGGAGAGGCCCTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGT 900

Qy       2016 GGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGC 2075
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGC 960

Qy       2076 ACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGGACAGCTGATCCAGGAGCCACG 2135
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGGACAGCTGATCCAGGAGCCACG 1020

Qy       2136 GGTCCTGCACTTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAG 2195
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGTCCTGCACTTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAG 1080

Qy       2196 CTCCCTGTGGAAGAGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTG 2255
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Db       1081 CTCCCTGTGGAAGAGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTG 1140

Qy       2256 GAATGGCACGCAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTCAGCCCCAGCAC 2315
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Qy       2316 TAGTGACCTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAG 2375
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Db       1201 TAGTGACCTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAG 1260

Qy       2376 CATCAACTTCAACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGA 2435
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CATCAACTTCAACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGA 1320

Qy       2436 AGCGGGGGTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCA 2495
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCGGGGGTCCCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCA 1380
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Qy       2496 GAAGATAATTTCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGC 2555
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Db       1381 GAAGATAATTTCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGC 1440

Qy       2556 CCAGAAACTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGC 2615
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CCAGAAACTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGC 1500

Qy       2616 CATGATCCTCAACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGC 2675
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Qy       2676 TGCAGCAGTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGA 2735
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TGCAGCAGTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGA 1620

Qy       2736 GTGCTGAGGCCGGCCAG 2752
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Db       1621 GTGCTGAGGCCGGCCAG 1637


RESULT 12
BD057525
LOCUS       BD057525               1787 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Netrin receptors.
ACCESSION   BD057525
VERSION     BD057525.1  GI:22603131
KEYWORDS    JP 2001505062-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 1787)
  AUTHORS   Lavigne,M.T., Leonardo,D.E., Hinck,L., Masu,M. and Masu,K.K.
  TITLE     Netrin receptors
  JOURNAL   Patent: JP 2001505062-A 2 17-APR-2001;
            THE REGENTS OF THE UNIV OF CALIFORNIA
COMMENT     PN   JP 2001505062-A/2
            PD   17-APR-2001
            PF   19-FEB-1998 JP 1998536840
            PR   19-FEB-1997 US    08/808982
            PI   MARC TESSIER LAVIGNE,DAVID E LEONARDO,LINDSAY HINCK,MASAYUKI
            PI   MASU,
            PI   KAZUKO KEINO MASU
            PC   C07K1/00,C07K14/00,C07K17/00,C07H21/02,C07H21/04,G01N33/53 CC
             Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .1787
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             56.8%;  Score 1562.4;  DB 6;  Length 1787;
  Best Local Similarity   98.5%;  Pred. No. 4.3e-252;
  Matches 1661;  Conservative    0;  Mismatches   16;  Indels    9;  Gaps    8;
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Qy       1070 GCAACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCT 1129
             ||||||||||||||||||||| ||||||| ||||||||||||||||||||||||||||||
Db          1 GCAACTGTACCAGTGACCTCTG-GTACACACTGCTTCTGGCCCTGAGGACGTGGCCCTCT 59

Qy       1130 ATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCTCATCCTCG 1189
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 ATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCTCATCCTCG 119

Qy       1190 TTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCT 1249
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 TTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCT 179

Qy       1250 CAGGCTTCCAGCCCGTCAGCATC-AAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACC 1308
             |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        180 CAGGCTTCCAGCCCGTCAGCATCTAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACC 239

Qy       1309 ATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAG 1368
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 ATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAG 299

Qy       1369 GATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGC 1428
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 GATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGC 359

Qy       1429 GGCCGCCACACACTGCACCACAGCTCTCCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGC 1488
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Db        360 GGCCGCCACACACTGCACCACAGCTCTCCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGC 419

Qy       1489 CTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGG 1548
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 CTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGG 479

Qy       1549 ACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATC 1608
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Db        480 ACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGAATCAGCCTCCTCATC 539

Qy       1609 CCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCG 1668
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 CCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCG 599

Qy       1669 GAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGT 1728
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 GAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGT 659

Qy       1729 GGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAG 1788
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Db        660 GGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAG 719

Qy       1789 CCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAG 1848
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Db        720 CCCAGCCCTGACAGCTGGAGCCTGGCCCTCAAAAAGCAGTCGTGCGAGGG-AGCTGGGAG 778

Qy       1849 GATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCC 1908
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Db        779 GATGT-CTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCC 837
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Qy       1909 AGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTC 1968
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        838 AGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTC 897

Qy       1969 AGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCC 2028
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 AGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCC 957

Qy       2029 CTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTG 2088
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 CTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTG 1017

Qy       2089 GTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTC 2148
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Db       1018 GTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTT- 1076

Qy       2149 AAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAG 2208
             ||||||||||||||||||||  |||    ||||||||||||||||||||||||||||||
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Qy       2209 AGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAG 2268
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Qy       2269 CGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTCAGCCCCAGCACTAGTGACCTGGCC 2328
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Qy       2329 TGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAAC 2388
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1255 TGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAAC 1314

Qy       2389 ATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCA 2448
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Db       1315 ATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCA 1374

Qy       2449 GCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCC 2508
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Db       1375 GCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCC 1434

Qy       2509 AGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAACTCCAC 2568
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1435 AGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAACTCCAC 1494

Qy       2569 CTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAAC 2628
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1495 CTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAAC 1554

Qy       2629 CTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCT 2688
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1555 CTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCT 1614

Qy       2689 GGACTGGGCCAGCCAGACGCTGGCCTC-TTCACAGTG-TCGGAGGCTGAGTGCTGAGGCC 2746
             ||    |||||||  ||||  ||||  ||  |||||||| ||||||||||||||||||||||
Db       1615 GGGACTGGCCAGCAGGACGGTGGCTTCTTTCACAGTGTTCGGAGGCTGAGTGCTGAGGCC 1674

Qy       2747 GGCCAG 2752
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Db       1675 GGCCAG 1680


RESULT 13
AX054976
LOCUS       AX054976                9700 bp    DNA     linear   PAT 13-JAN-2001
DEFINITION  Sequence 91 from Patent WO0073328.
ACCESSION   AX054976
VERSION     AX054976.1  GI:12228344
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   van Criekinge,W., Roelens,I., Bogaert,T. and Verwaerde,P.
  TITLE     Unc-5 constructs and screening methods
  JOURNAL   Patent: WO 0073328-A 91 07-DEC-2000;
            Devgen NV (BE)
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
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ORIGIN

  Query Match             47.4%;  Score 1304.2;  DB 6;  Length 9700;
  Best Local Similarity   99.8%;  Pred. No. 6.8e-209;
  Matches 1306;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1437 CACACTGCACCACAGCTCTCCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCAC 1496
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Qy       1497 CCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAA 1556
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Db         67 CCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAA 126

Qy       1557 CTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCCAGA 1616
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Db        127 CTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGAATCAGCCTCCTCATCCCCCCAGA 186

Qy       1617 TGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGT 1676
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Db        187 TGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGT 246

Qy       1677 GAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCC 1736
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Db        247 GAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCC 306

Qy       1737 TGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCC 1796
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCC 366

Qy       1797 TGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCT 1856
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        367 TGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCT 426

Qy       1857 GCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTG 1916
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Db        427 GCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTG 486

Qy       1917 CTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGC 1976
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 CTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGC 546

Qy       1977 TGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTA 2036
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2037 CAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCT 2096
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 CAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCT 666

Qy       2097 GGAGAAGCAGCTGGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGACAG 2156
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Qy       2157 TTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCT 2216
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Qy       2217 CCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTT 2276
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 CCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTT 846

Qy       2277 GCACTGCACCTTCACCCTGGAGCGTGTCAGCCCCAGCACTAGTGACCTGGCCTGCAAGCT 2336
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Qy       2397 GGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGT 2456
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        967 GGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCAAGCCCTGGT 1026

Qy       2457 GGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGA 2516
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Db       1027 GGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGA 1086

Qy       2517 CCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAACTCCACCTGGACAG 2576
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Db       1087 CCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAACTCCACCTGGACAG 1146

Qy       2577 CCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGA 2636
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Db       1147 CCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGA 1206

Qy       2637 GGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGG 2696
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2697 CCAGCCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGAGGC 2745
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Db       1267 CCAGCCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGAGTC 1315
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RESULT 14
MMU72634
LOCUS       MMU72634                9299 bp    mRNA    linear   ROD 13-MAY-1997
DEFINITION  Mus musculus rostral cerebellar malformation protein (rcm) mRNA,
            complete cds.
ACCESSION   U72634
VERSION     U72634.1  GI:2088526
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 9299)
  AUTHORS   Ackerman,S.L., Kozak,L.P., Przyborski,S.A., Rund,L.A., Boyer,B.B.
            and Knowles,B.B.
  TITLE     The mouse rostral cerebellar malformation gene encodes an
            UNC-5-like protein
  JOURNAL   Nature 386 (6627), 838-842 (1997)
  MEDLINE   97271898
   PUBMED   9126743
REFERENCE   2  (bases 1 to 9299)
  AUTHORS   Ackerman,S.L., Kozak,L.P., Rund,L.A. and Knowles,B.B.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-SEP-1996) The Jackson Laboratory, 600 Main Street,
            Bar Harbor, ME 04609, USA
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ORIGIN

Query Match 36.0%; Score 992; DB 10; Length 9299;
Best Local Similarity 62.7%; Pred. No. 1.5e-156;
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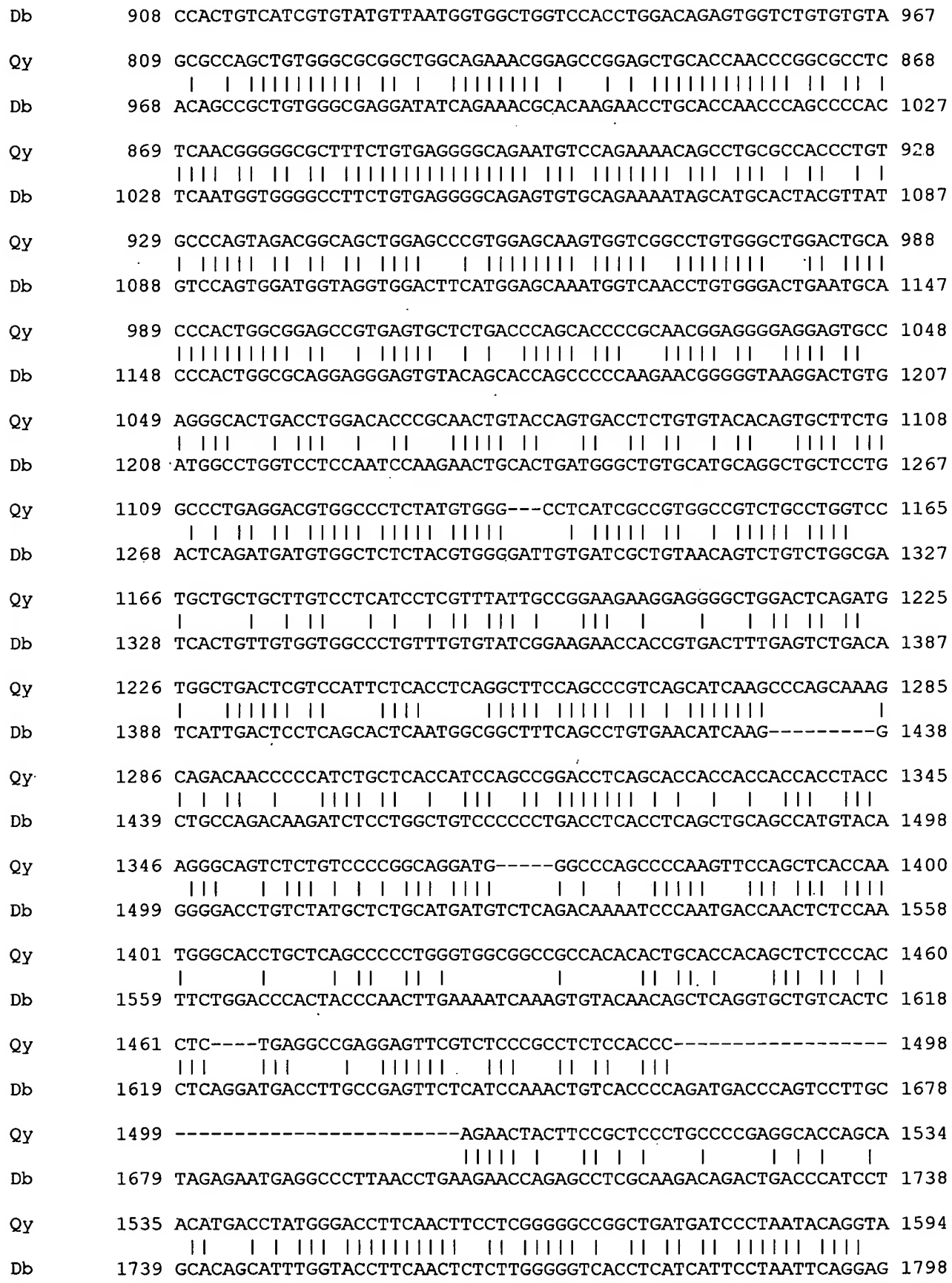

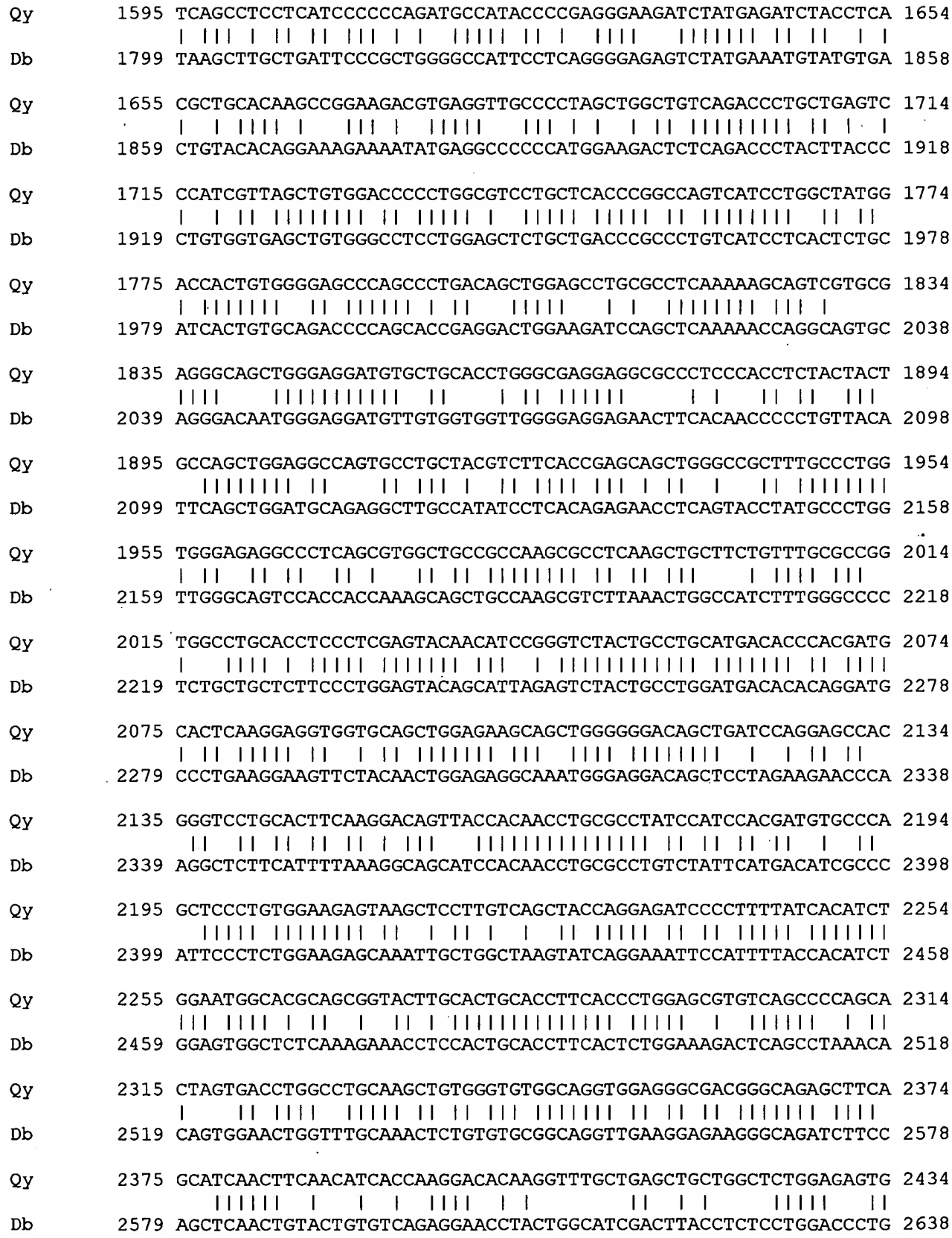

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VERSION     AY187310.1  GI:31442350
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            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 2962)
  AUTHORS   Guan,W. and Condic,M.L.
  TITLE     Characterization of Netrin-1, Neogenin and cUNC-5H3 expression
            during chick dorsal root ganglia development
  JOURNAL   Gene Expr. Patterns 3, 369-373 (2003)
REFERENCE   2  (bases 1 to 2962)
  AUTHORS   Guan,W. and Condic,M.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-NOV-2002) Neurobiology & Anatomy, University of Utah,
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ORIGIN

Query Match 36.0%; Score 991; DB 5; Length 2962;
Best Local Similarity 62.6%; Pred. No. 2.6e-156;
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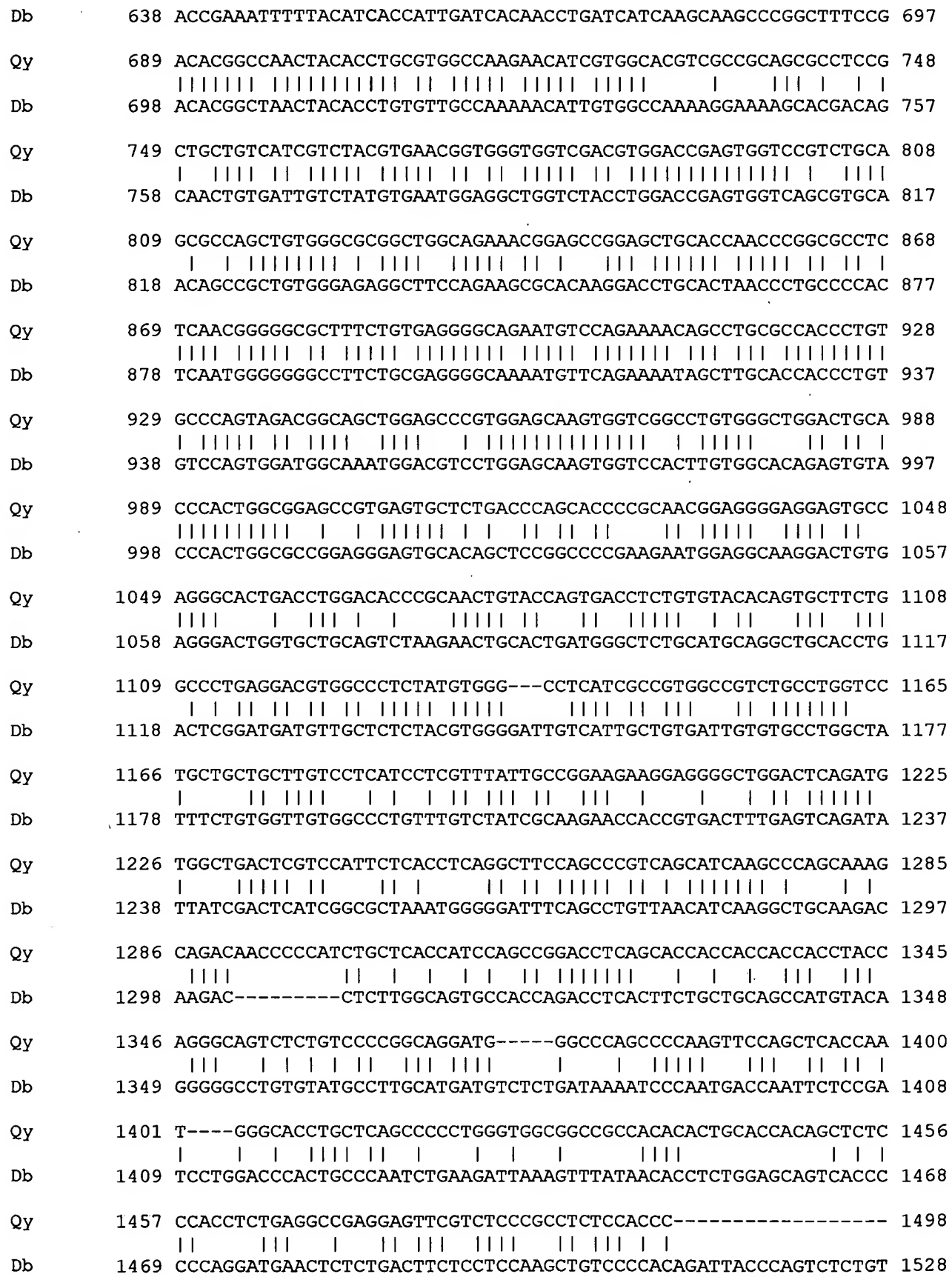

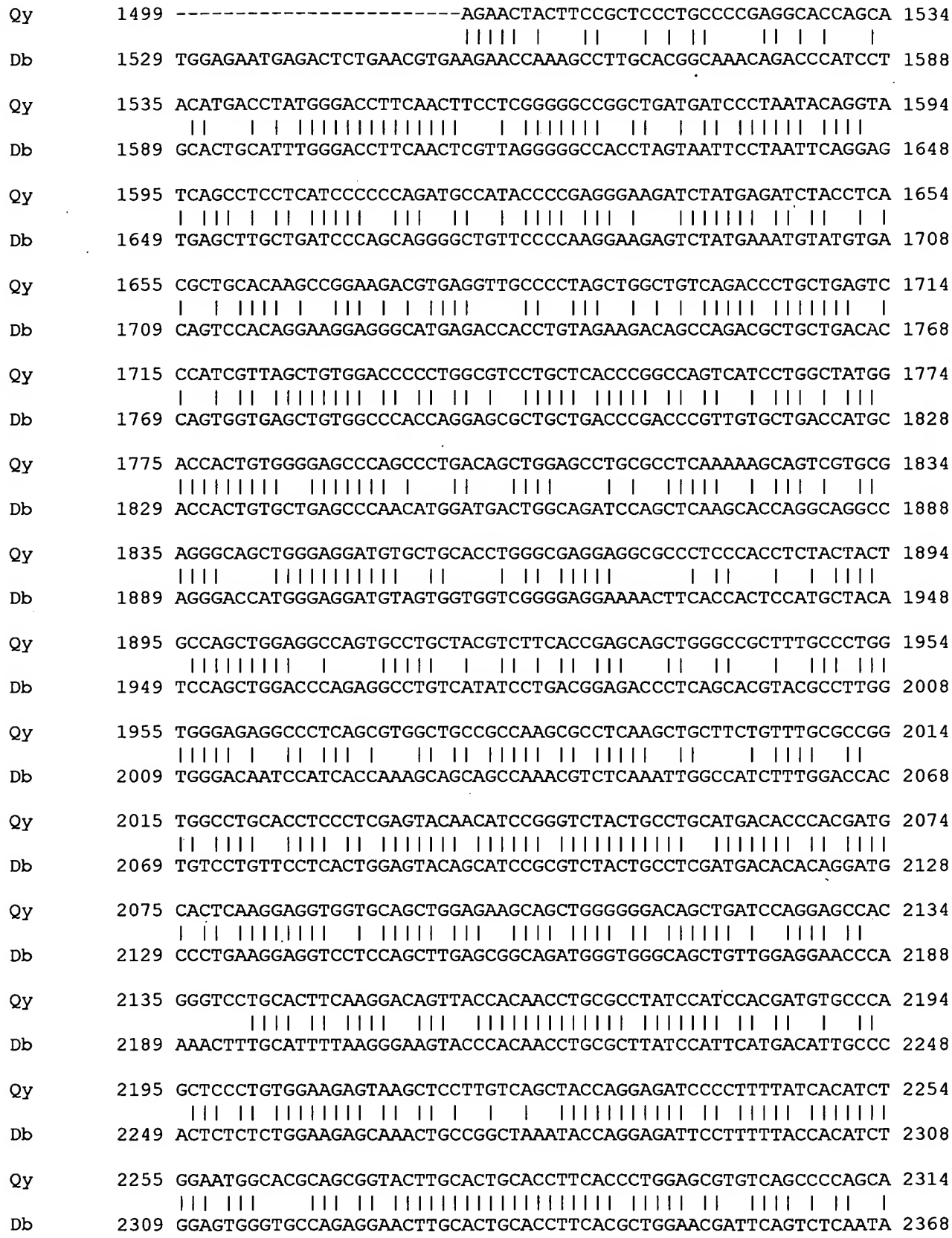

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 5, 2005, 14:42:51 ; Search time 1401 Seconds
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Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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23	2328	84.6	2575	12	ADH71621	Adh71621 Human gen
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ALIGNMENTS

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AC ABK37922;
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DT 21-MAY-2002 (first entry)
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KW Human; NOVX; ss; gene; cardiomyopathy; atherosclerosis; diabetes;

KW cell signal processing disorder; metabolic disorder; obesity; infection;
KW anorexia; cancer-associated cachexia; cancer; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorders; dyslipidaemia; pain; asthma; hypertension;
KW osteoporosis; Crohn's disease; multiple sclerosis; angina pectoris;
KW myocardial infarction; ulcer; allergy; benign prostatic hypertrophy;
KW psychosis; neurological disorder; anxiety; schizophrenia;
KW manic depression; dementia; dyskinesia; Huntington's disease;
KW Gilles de la Tourette's syndrome; gene therapy.
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XX
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XX
PD 07-FEB-2002.
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PF 30-JUL-2001; 2001WO-US024225.
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PR 28-JUL-2000; 2000US-0221409P.
PR 04-AUG-2000; 2000US-0222840P.
PR 04-AUG-2000; 2000US-0223752P.
PR 04-AUG-2000; 2000US-0223762P.
PR 04-AUG-2000; 2000US-0223769P.
PR 04-AUG-2000; 2000US-0223770P.
PR 14-AUG-2000; 2000US-0225146P.
PR 15-AUG-2000; 2000US-0225392P.
PR 15-AUG-2000; 2000US-0225470P.
PR 16-AUG-2000; 2000US-0225697P.
PR 01-FEB-2001; 2001US-0263662P.
PR 05-APR-2001; 2001US-0281645P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Padigaru M, Mezes P, Mishra V, Burgess C, Casman S, Grosse WM;
PI Alsobrook JP, Lepley DM, Gerlach VL, Macdougall JR, Smithson G;
XX
DR WPI; 2002-180074/23.
DR P-PSDB; AAU85403.
XX
PT New isolated cytoplasmic, nuclear, membrane bound, or secreted
PT polypeptide, useful for treating cardiomyopathy, atherosclerosis,
PT infections, cancer, neurodegenerative, metabolic, hematopoietic and
PT immune disorders.
XX
PS Claim 9; Page 9-10; 213pp; English.
XX
CC The invention relates to an isolated cytoplasmic, nuclear, membrane
CC bound, or secreted polypeptide (NOVX, x= 1-14) their variants or mature
CC form. Also included are the nucleic acids encoding the NOVX proteins, a
CC vector comprising the nucleic acid, a cell comprising the vector, an anti
CC -NOVX antibody and modulators of NOVX. NOVX, the nucleic acid and the
CC antibody are useful for treating or preventing a NOVX-associated
CC disorder, where the disorder is selected from cardiomyopathy,
CC atherosclerosis, diabetes, a disorder related to cell signal processing
CC and metabolic pathway modulation, metabolic disorders, obesity,
CC infectious disease, anorexia, cancer-associated cachexia, cancer,
CC neurodegenerative disorders, Alzheimer's disease, Parkinson's disease,

CC immune disorders, haematopoietic disorders, and the various
CC dyslipidaemias, metabolic disturbances associated with obesity, the
CC metabolic syndrome X and wasting disorders associated with chronic
CC diseases, bacterial, fungal, protozoal and viral infections, pain,
CC bulimia, asthma, hypertension, urinary retention, osteoporosis, Crohn's
CC disease, multiple sclerosis, Albright Hereditary Osteodystrophy, angina
CC pectoris, myocardial infarction, ulcer, allergy, benign prostatic
CC hypertrophy, and psychotic and neurological disorders, including anxiety,
CC schizophrenia, manic depression, delirium, dementia, and dyskinesias,
CC such as Huntington's disease and Gilles de la Tourette's syndrome. The
CC nucleic acid is useful in gene therapy. The present sequence encodes a
CC NOVX protein
XX
SQ Sequence 2752 BP; 505 A; 937 C; 829 G; 481 T; 0 U; 0 Other;

Query Match 100.0%; Score 2752; DB 6; Length 2752;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CCGCGGGGCCCCGCGCCCGGCCCGCCCGCCTGCCCGCCCGCGGCCATGGCCGTCCGGCCC 60
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Db          1 CCGCGGGGCCCCGCGCCCGGCCCGCCCGCCTGCCCGCCCGCGGCCATGGCCGTCCGGCCC 60

Qy         61 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 120
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Qy        121 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC 180
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Qy        181 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 240
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Db        181 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 240

Qy        241 AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 300
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Db        241 AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 300

Qy        301 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGC 360

Qy        361 ATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCGGGCTGGAGGAATACTGGTGCCAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCGGGCTGGAGGAATACTGGTGCCAG 420

Qy        421 TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 480

Qy        481 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 540

Qy        541 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        541 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600

Qy        601 AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 660

Qy        661 CTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAAC 720

Qy        721 ATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGG 780

Qy        781 TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG 840

Qy        841 AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT 900

Qy        901 GTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGGAGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGGAGC 960

Qy        961 AAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCA 1020

Qy       1021 GCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACC 1080

Qy       1081 AGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTC 1140
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Db       1081 AGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTC 1140

Qy       1141 ATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCTCATCCTCGTTTATTGCCGG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCTCATCCTCGTTTATTGCCGG 1200

Qy       1201 AAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTCCAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTCCAG 1260

Qy       1261 CCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCGGAC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCGGAC 1320

Qy       1321 CTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCCAGC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCCAGC 1380

Qy       1381 CCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACACA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACACA 1440
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Qy       1441 CTGCACCACAGCTCTCCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAG 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CTGCACCACAGCTCTCCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAG 1500

Qy       1501 AACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTC 1560
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Db       1501 AACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTC 1560

Qy       1561 CTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCCAGATGCC 1620
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Db       1561 CTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCCAGATGCC 1620

Qy       1621 ATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGG 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 ATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGG 1680

Qy       1681 TTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCTGGC 1740
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Db       1681 TTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCTGGC 1740

Qy       1741 GTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGAC 1800
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Db       1741 GTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGAC 1800

Qy       1801 AGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCAC 1860
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Db       1801 AGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCAC 1860

Qy       1861 CTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTAC 1920
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Db       1861 CTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTAC 1920

Qy       1921 GTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCC 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 GTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCC 1980

Qy       1981 GCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAAC 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 GCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAAC 2040

Qy       2041 ATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAG 2100
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Db       2041 ATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAG 2100

Qy       2101 AAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGACAGTTAC 2160
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Db       2101 AAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGACAGTTAC 2160

Qy       2161 CACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTT 2220
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Db       2161 CACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTT 2220

Qy       2221 GTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCAC 2280
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Db       2221 GTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCAC 2280
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Qy       2281 TGCACCTTCACCCTGGAGCGTGTCAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGG 2340
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Db       2281 TGCACCTTCACCCTGGAGCGTGTCAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGG 2340

Qy       2341 GTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAGGAC 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 GTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAGGAC 2400

Qy       2401 ACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGC 2460
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Db       2401 ACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGC 2460

Qy       2461 CCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGACCCA 2520
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Qy       2521 CCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAACTCCACCTGGACAGCCAT 2580
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Db       2521 CCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAACTCCACCTGGACAGCCAT 2580

Qy       2581 CTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCG 2640
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Db       2581 CTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCG 2640

Qy       2641 CGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAG 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 CGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAG 2700

Qy       2701 CCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGAGGCCGGCCAG 2752
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Db       2701 CCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGAGGCCGGCCAG 2752
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RESULT 2
ADH71617
ID ADH71617 standard; DNA; 2752 BP.
XX
AC ADH71617;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human gene of the invention NOV21e SEQ ID NO:513.
XX
KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
PF 03-JUN-2003; 2003WO-US017430.
XX

PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
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PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0386942P.
PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
PR 13-AUG-2002; 2002US-0403459P.
PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.

PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX
DR WPI; 2004-081935/08.
DR P-PSDB; ADH71618.
XX
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
PS Example 21; SEQ ID NO 513; 1880pp; English.
XX
CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX

SQ Sequence 2752 BP; 505 A; 937 C; 829 G; 481 T; 0 U; 0 Other;

Query Match 100.0%; Score 2752; DB 12; Length 2752;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CCGCGGGGCCCCGCGCCCGGCCCGCCCGCCTGCCCGCCCGCGGCCATGGCCGTCCGGCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGCGGGGCCCCGCGCCCGGCCCGCCCGCCTGCCCGCCCGCGGCCATGGCCGTCCGGCCC 60

Qy         61 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC 180

Qy        181 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 240

Qy        241 AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 300

Qy        301 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGC 360

Qy        361 ATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCGGGCTGGAGGAATACTGGTGCCAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCGGGCTGGAGGAATACTGGTGCCAG 420

Qy        421 TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 480

Qy        481 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 540

Qy        541 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600

Qy        601 AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 660

Qy        661 CTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAAC 720

Qy        721 ATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGG 780
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Qy        781 TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG 840

Qy        841 AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT 900

Qy        901 GTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGGAGC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGGAGC 960

Qy        961 AAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGACCCA 1020

Qy       1021 GCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGTACC 1080

Qy       1081 AGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGCCTC 1140

Qy       1141 ATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCTCATCCTCGTTTATTGCCGG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCTCATCCTCGTTTATTGCCGG 1200

Qy       1201 AAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTCCAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTCCAG 1260

Qy       1261 CCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCGGAC 1320
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Db       1261 CCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCGGAC 1320

Qy       1321 CTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCCAGC 1380
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Db       1321 CTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCCAGC 1380

Qy       1381 CCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACACA 1440
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Db       1381 CCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCACACA 1440

Qy       1441 CTGCACCACAGCTCTCCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAG 1500
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Qy       1501 AACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTC 1560
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Qy       1561 CTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCCAGATGCC 1620
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Db       1561 CTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCCAGATGCC 1620
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Qy       1621 ATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGG 1680
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Db       1621 ATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTGAGG 1680

Qy       1681 TTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCTGGC 1740
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Db       1681 TTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCTGGC 1740

Qy       1741 GTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGAC 1800
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Db       1741 GTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCTGAC 1800

Qy       1801 AGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCAC 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 AGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGGATGTGCTGCAC 1860

Qy       1861 CTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTAC 1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCCTGCTAC 1920

Qy       1921 GTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCC 1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 GTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCC 1980

Qy       1981 GCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAAC 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 GCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAAC 2040

Qy       2041 ATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAG 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 ATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAG 2100

Qy       2101 AAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGACAGTTAC 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 AAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGACAGTTAC 2160

Qy       2161 CACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTT 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 CACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAGCTCCTT 2220

Qy       2221 GTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCAC 2280
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Db       2221 GTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTACTTGCAC 2280

Qy       2281 TGCACCTTCACCCTGGAGCGTGTCAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGG 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 TGCACCTTCACCCTGGAGCGTGTCAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGG 2340

Qy       2341 GTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAGGAC 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 GTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACCAAGGAC 2400

Qy       2401 ACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGC 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 ACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTGGTGGGC 2460

Qy       2461 CCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGACCCA 2520
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2461 CCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTGGACCCA 2520

Qy        2521 CCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAACTCCACCTGGACAGCCAT 2580
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2521 CCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAACTCCACCTGGACAGCCAT 2580

Qy        2581 CTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCG 2640
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2581 CTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCG 2640

Qy        2641 CGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAG 2700
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2641 CGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTGGGCCAG 2700

Qy        2701 CCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGAGGCCGGCCAG 2752
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2701 CCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGAGGCCGGCCAG 2752
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RESULT 3
ABK52891
ID   ABK52891 standard; DNA; 2697 BP.
XX
AC   ABK52891;
XX
DT   27-AUG-2002  (first entry)
XX
DE   Human netrin binding membrane receptor UNC5H-1 DNA sequence #1.
XX
KW   Netrin binding membrane receptor; receptor; UNC5H-1; gene; ds; human;
KW   nootropic; neuroprotective; cytostatic; antiparkinsonian;
KW   cerebroprotective; cancer; central nervous system; CNS; stroke;
KW   Parkinson's disease; multiple sclerosis; Alzheimer's disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .2697
FT                   /*tag=  a
FT                   /product= "Netrin binding membrane receptor UNC5H-1"
XX
PN   WO200233080-A2.
XX
PD   25-APR-2002.
XX
PF   15-OCT-2001; 2001WO-EP011891.
XX
PR   16-OCT-2000; 2000US-0240061P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Koehler RH;
XX
DR   WPI; 2002-463314/49.
DR   P-PSDB; AAU97899.
XX
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PT Novel human netrin binding membrane receptor polypeptide and
PT polynucleotides for identifying modulating agents useful in treating
PT diseases e.g. Parkinson's disease, multiple sclerosis, stroke,
PT Alzheimer's disease.
XX
PS Claim 1; Fig 1; 94pp; English.
XX
CC This invention relates to the DNA and protein sequences of a novel
CC purified human netrin binding membrane receptor, UNC5H-1. The DNA
CC sequence of the invention is useful as a probe for detecting a nucleic
CC acid encoding the UNC5H-1 protein in a biological sample. The sequences
CC of the invention are useful to screen for agents which decrease the
CC activity of the UNC5H-1 protein. The sequences are also useful for
CC screening agents which regulate (modulate) the activity of the protein of
CC the invention. A pharmaceutical composition containing the protein of the
CC invention or a reagent that modulates the activity of the UNC5H-1 protein
CC may be useful for treating a UNC5H-1 dysfunction related disease such as
CC cancer or a central nervous system (CNS) disorders (e.g, Parkinson's
CC disease, multiple sclerosis, stroke and Alzheimer's disease). Fusion
CC proteins comprising the UNC5H-1 protein are useful for generating
CC antibodies and for in various assay systems, and the protein can be used
CC as a bait protein in a two-hybrid assay or three-hybrid assay. The method
CC of the invention is useful for detecting a coding sequence for the UNC5H-
CC 1 protein. The present sequence represents a DNA sequence encoding the
CC human netrin binding membrane receptor UNC5H-1 protein of the invention
XX
SQ Sequence 2697 BP; 503 A; 906 C; 807 G; 481 T; 0 U; 0 Other;

Query Match 97.7%; Score 2687.4; DB 6; Length 2697;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2691; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy      46 ATGGCCGTCCGGCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTC 105
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGGCCGTCCGGCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTC 60

Qy     106 CGCGGCTCGGGTGCCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCG 165
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CGCGGCTCGGGTGCCCAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCG 120

Qy     166 GACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCA 225
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GACCTGCTTCCCCACTTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCA 180

Qy     226 GTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAG 285
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAG 240

Qy     286 TGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCC 345
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 TGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCC 300

Qy     346 ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCGGGCTGGAG 405
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 ACCATGGAGGTCCGCATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCGGGCTGGAG 360

Qy     406 GAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC 465
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAATACTGGTGCCAGTGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCC 420

Qy        466 TACATCCGCATAGCCAGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG 525
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Db        421 TACATCCGCATAGCCTATTTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTG 480

Qy        526 TCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAG 585
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAG 540

Qy        586 GTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATC 645
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATC 600

Qy        646 ACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACC 705
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACGCGGGAGCACAGCCTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACC 660

Qy        706 TGCGTGGCCAAGAACATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTCATCGTCTAC 765
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGCGTGGCCAAGAACATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTCATCGTCTAC 720

Qy        766 GTGAACGGTGGGTGGTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGC 825
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTGAACGGTGGGTGGTCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGC 780

Qy        826 GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTC 885
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGCTGGCAGAAACGGAGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTC 840

Qy        886 TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGC 945
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        841 TGTGAGGGGCAGAATGTCCAGAAAACAGCCTGCGCCACCCTGTGCCCAGTGGACGGCAGC 900

Qy        946 TGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGT 1005
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Db        901 TGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGT 960

Qy       1006 GAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGAC 1065
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGAC 1020

Qy       1066 ACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCC 1125
                |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       1021 ACCCGCAACTGTACCAGTGACCTCTGTGTACACACTGCTTCTGGCCCTGAGGACGTGGCC 1080

Qy       1126 CTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCTCATC 1185
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCTCATC 1140

Qy       1186 CTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTC 1245
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTC 1200

Qy       1246 ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTC 1305
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1201 ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTC 1260

Qy       1306 ACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGG 1365
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 ACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGG 1320

Qy       1366 CAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGT 1425
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGT 1380

Qy       1426 GGCGGCCGCCACACACTGCACCACAGCTCTCCCACCTCTGAGGCCGAGGAGTTCGTCTCC 1485
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GGCGGCCGCCACACACTGCACCACAGCTCTCCCACCTCTGAGGCCGAGGAGTTCGTCTCC 1440

Qy       1486 CGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTAT 1545
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTAT 1500

Qy       1546 GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTC 1605
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Db       1501 GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGAATCAGCCTCCTC 1560

Qy       1606 ATCCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG 1665
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATCCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG 1620

Qy       1666 CCGGAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGC 1725
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 CCGGAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGC 1680

Qy       1726 TGTGGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGG 1785
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 TGTGGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGG 1740

Qy       1786 GAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG 1845
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 GAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG 1800

Qy       1846 GAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAG 1905
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Db       1801 GAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAG 1860

Qy       1906 GCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCC 1965
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 GCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCC 1920

Qy       1966 CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC 2025
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC 1980

Qy       2026 TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG 2085
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG 2040

Qy       2086 GTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCAC 2145
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 GTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCAC 2100
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Qy       2146 TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGG 2205
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGG 2160

Qy       2206 AAGAGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACG 2265
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 AAGAGTAAGCTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACG 2220

Qy       2266 CAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTCAGCCCCAGCACTAGTGACCTG 2325
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 CAGCGGTACTTGCACTGCACCTTCACCCTGGAGCGTGTCAGCCCCAGCACTAGTGACCTG 2280

Qy       2326 GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTC 2385
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 GCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTC 2340

Qy       2386 AACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTC 2445
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 AACATCACCAAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTC 2400

Qy       2446 CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATT 2505
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 CCAGCCCTGGTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATT 2460

Qy       2506 TCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAACTC 2565
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Db       2461 TCCAGCCTGGACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAACTC 2520

Qy       2566 CACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTC 2625
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 CACCTGGACAGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTC 2580

Qy       2626 AACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTG 2685
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 AACCTGTGGGAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTG 2640

Qy       2686 GCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGA 2742
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 GCTGGACTGGGCCAGCCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGA 2697
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RESULT 4
ABK49422
ID ABK49422 standard; DNA; 2881 BP.
XX
AC ABK49422;
XX
DT 15-JUL-2002 (first entry)
XX
DE DNA encoding human UNC5-like protein NOV1.
XX
KW Human; NOVX polypeptide; cardiomyopathy; atherosclerosis; cancer;
KW cell signal processing; metabolic pathway modulation; cancerous tissue;
KW antibody; diabetes; transgenic animal; UNC5-like protein; NOV1;
KW chromosome 13; gene; ds.
XX

OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 87. .2786
FT /*tag= a
FT /product= "Human UNC5-like protein NOV1"
XX
PN WO200229038-A2.
XX
PD 11-APR-2002.
XX
PF 04-OCT-2001; 2001WO-US031377.
XX
PR 04-OCT-2000; 2000US-0237862P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Herrmann JL, Rastelli L, Shimkets RA;
XX
DR WPI; 2002-340104/37.
DR P-PSDB; AAU79939.
XX
PT Novel isolated NOVX polypeptide, and encoded polynucleotide, useful for
PT treating cardiomyopathy, artherosclerosis, and cancer.
XX
PS Claim 8; Page 7-8; 180pp; English.
XX
CC The present invention relates to a new NOVX polypeptide having a 900
CC (NOV1), 4349 (NOV2), 940 (NOV3), 798 (NOV4), 865 (NOV5), or 331 (NOV6)
CC residue amino acid sequence, as given in the specification. The novel
CC polypeptide, and its encoding polynucleotide, are used to treat
CC cardiomyopathy, atherosclerosis, cancer or a disease related to cell
CC signal processing and metabolic pathway modulation, in a human. Detecting
CC the polypeptide or polynucleotide is useful for identifying cancerous
CC tissue. The antibody can be used to treat diabetes or cancer. The host
CC cells can be used to produce non-human transgenic animals useful in drug
CC screening. The present nucleic acid sequence is that of the human UNC5-
CC like NOV1 gene located on chromosome 13. This sequence encodes the human
CC UNC5-like protein NOV1 of the invention
XX
SQ Sequence 2881 BP; 526 A; 985 C; 868 G; 502 T; 0 U; 0 Other;

Query Match 97.3%; Score 2676.4; DB 6; Length 2881;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2728; Conservative 0; Mismatches 21; Indels 9; Gaps 3;

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Qy          1 CCGCGGGGCCCCGCGCCCGGCCCGCCCGCCTGCCCGCCCGCGGCCATGGCCGTCCGGCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         42 CCGCGGGGCCCCGCGCCCGGCCCGCCCGCCTGCCCGCCCGCGGCCATGGCCGTCCGGCCC 101

Qy         61 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 161

Qy        121 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC 221
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Qy        181 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 281

Qy        241 AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 341

Qy        301 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGC 360
              |||||||||||||||||||||||||||||||||||   ||| ||||||||||||||||
Db        342 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGTGAGCCGACCATGGAGGTCCGC 401

Qy        361 ATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCGGGCTGGAGGAATACTGGTGCCAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        402 ATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCGGGCTGGAGGAATACTGGTGCCAG 461

Qy        421 TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        462 TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 521

Qy        481 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        522 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 581

Qy        541 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        582 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 641

Qy        601 AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        642 AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 701

Qy        661 CTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        702 CTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAAC 761

Qy        721 ATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        762 ATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGG 821

Qy        781 TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        822 TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG 881

Qy        841 AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        882 AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT 941

Qy        901 GTCCAGAA---AACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGG 957
              |||||  |    || | || | |    ||   | | || ||||||||||||||||||
Db        942 GTCCATGACCGCACCGTCTCCTCTCTGCTTGTCTCTGTGGACGGCAGCTGGAGCCCGTGG 1001

Qy        958 AGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGAC 1017
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1002 AGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGAC 1061
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Qy       1018 CCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGT 1077
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1062 CCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGT 1121

Qy       1078 ACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGC 1137
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1122 ACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGC 1181

Qy       1138 CTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCTCATCCTCGTTTATTGC 1197
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Db       1182 CTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCTCATCCTCGTTTATTGC 1241

Qy       1198 CGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTC 1257
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Db       1242 CGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTC 1301

Qy       1258 CAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCG 1317
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Db       1302 CAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCG 1361

Qy       1318 GACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCC 1377
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Db       1362 GACCTCAG---CACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCC 1418

Qy       1378 AGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCAC 1437
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Db       1419 AGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCAC 1478

Qy       1438 ACACTGCACCACAGCTCTCCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACC 1497
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Db       1479 ACACTGCACCACAGCTCTCCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACC 1538

Qy       1498 CAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAAC 1557
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Db       1539 CAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAAC 1598

Qy       1558 TTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCCAGAT 1617
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Qy       1618 GCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTG 1677
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Db       1659 GCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTG 1718

Qy       1678 AGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCT 1737
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Db       1719 AGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCT 1778

Qy       1738 GGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCT 1797
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Db       1779 GGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCT 1838

Qy       1798 GACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGG---AGGATGTG 1854
             ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||||
Db       1839 GACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGCAGGATGTG 1898

Qy       1855 CTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCC 1914
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Db       1899 CTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCC 1958

Qy       1915 TGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTG 1974

Db       1959 TGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTG 2018

Qy       1975 GCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAG 2034

Db       2019 GCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAG 2078

Qy       2035 TACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAG 2094

Db       2079 TACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAG 2138

Qy       2095 CTGGAGAAGCAGCTGGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGAC 2154

Db       2139 CTGGAGAAGCAGCTGGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGAC 2198

Qy       2155 AGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAG 2214

Db       2199 AGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAG 2258

Qy       2215 CTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTAC 2274

Db       2259 CTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTAC 2318

Qy       2275 TTGCACTGCACCTTCACCCTGGAGCGTGTCAGCCCCAGCACTAGTGACCTGGCCTGCAAG 2334

Db       2319 TTGCACTGCACCTTCACCCTGGAGCGTGTCAGCCCCAGCACTAGTGACCTGGCCTGCAAG 2378

Qy       2335 CTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACC 2394

Db       2379 CTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACC 2438

Qy       2395 AAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTG 2454

Db       2439 AAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTG 2498

Qy       2455 GTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTG 2514

Db       2499 GTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTG 2558

Qy       2515 GACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAACTCCACCTGGAC 2574

Db       2559 GACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAACTCCACCTGGAC 2618

Qy       2575 AGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGG 2634

Db       2619 AGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGG 2678

Qy       2635 GAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTG 2694

Db       2679 GAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTG 2738

Qy       2695 GGCCAGCCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGAGGCCGGCCAG 2752
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Db 2739 GGCCAGCCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGAGGCCGGCCAG 2796

RESULT 5
ADH71609
ID ADH71609 standard; DNA; 2881 BP.
XX
AC ADH71609;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human gene of the invention NOV21a SEQ ID NO:505.
XX
KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
PF 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386931P.
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PR 07-JUN-2002; 2002US-0386971P.
PR 07-JUN-2002; 2002US-0387262P.
PR 08-JUN-2002; 2002US-0296960P.
PR 10-JUN-2002; 2002US-0387400P.
PR 10-JUN-2002; 2002US-0387535P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.
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PR 19-JUN-2002; 2002US-0390006P.
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PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
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PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403448P.
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PA (CURA-) CURAGEN CORP.
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PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;

PI Zhong H;
XX
DR WPI; 2004-081935/08.
DR P-PSDB; ADH71610.
XX
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
PS Example 21; SEQ ID NO 505; 1880pp; English.
XX
CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
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SQ Sequence 2881 BP; 526 A; 985 C; 868 G; 502 T; 0 U; 0 Other;

Query Match 97.3%; Score 2676.4; DB 12; Length 2881;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2728; Conservative 0; Mismatches 21; Indels 9; Gaps 3;

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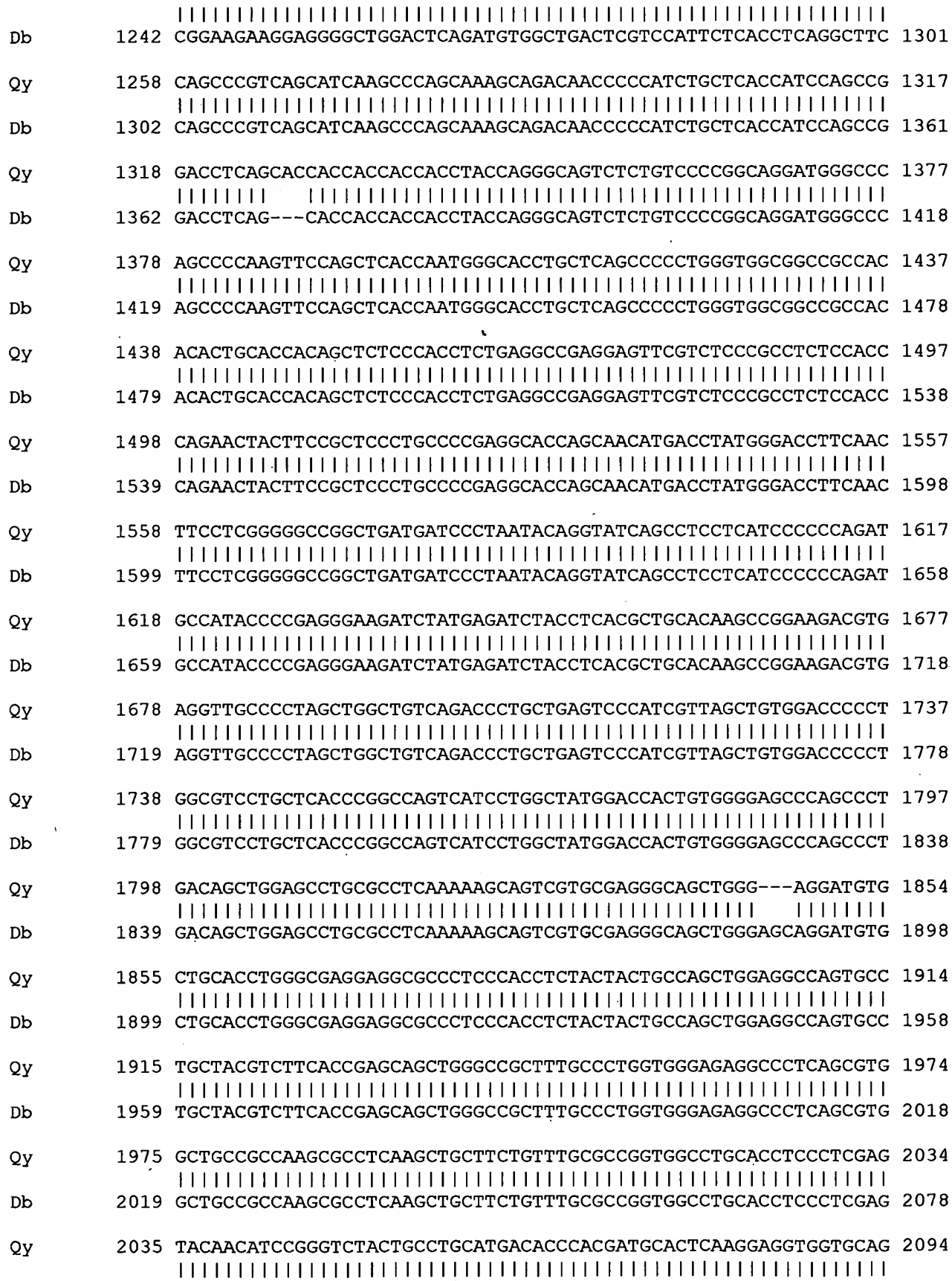

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RESULT 6
ADH71649
ID   ADH71649 standard; DNA; 2881 BP.
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AC   ADH71649;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Human gene of the invention NOV21u SEQ ID NO:545.
XX
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KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003102155-A2.
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PD 11-DEC-2003.
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XX
PR 03-JUN-2002; 2002US-0385120P.
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PR 20-SEP-2002; 2002US-0412528P.
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PR 05-NOV-2002; 2002US-00423798.
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XX
PA (CURA-) CURAGEN CORP.
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PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
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PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX
DR WPI; 2004-081935/08.
DR P-PSDB; ADH71650.
XX
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
PS Example 21; SEQ ID NO 545; 1880pp; English.
XX
CC The invention relates to a novel isolated polypeptide (NOVX). A
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CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 2881 BP; 526 A; 986 C; 868 G; 501 T; 0 U; 0 Other;

Query Match 97.2%; Score 2674.8; DB 12; Length 2881;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2727; Conservative 0; Mismatches 22; Indels 9; Gaps 3;

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Db         42 CCGCGGGGCCCCGCGCCCGGCCCGCCCGCCTGCCCGCCCGCGGCCATGGCCGTCCGGCCC 101

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Qy        721 ATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGG 780
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Db        762 ATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGG 821

Qy        781 TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG 840
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Db        822 TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG 881

Qy        841 AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT 900
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Db        882 AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT 941

Qy        901 GTCCAGAA---AACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGG 957
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Db        942 GTCCATGACCGCACCGTCTCCTCTCTGCTTGTCTCTGTGGACGGCAGCTGGAGCCCGTGG 1001

Qy        958 AGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGAC 1017
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1002 AGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGAC 1061

Qy       1018 CCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGT 1077
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Db       1062 CCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGT 1121

Qy       1078 ACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGC 1137
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1122 ACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGC 1181

Qy       1138 CTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCTCATCCTCGTTTATTGC 1197
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Db       1182 CTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCTCATCCTCGTTTATTGC 1241

Qy       1198 CGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTC 1257
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1242 CGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTC 1301

Qy       1258 CAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCG 1317
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1302 CAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCG 1361

Qy       1318 GACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCC 1377
                ||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1362 GACCTCAG---CACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCC 1418

Qy       1378 AGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCAC 1437
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1419 AGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCAC 1478

Qy       1438 ACACTGCACCACAGCTCTCCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACC 1497
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 ACACTGCACCACAGCTCTCCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACC 1538

Qy       1498 CAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAAC 1557
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Db       1539 CAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAAC 1598

Qy       1558 TTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCCAGAT 1617
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Db       1599 TTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCCAGAT 1658

Qy       1618 GCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTG 1677
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Db       1659 GCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTG 1718

Qy       1678 AGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCT 1737
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Db       1719 AGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCT 1778

Qy       1738 GGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCT 1797
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Db       1779 GGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCT 1838

Qy       1798 GACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGG---AGGATGTG 1854
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Qy       1855 CTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCC 1914
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Db       1899 CTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCC 1958

Qy       1915 TGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTG 1974
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Db       1959 TGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTG 2018

Qy       1975 GCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAG 2034
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Db       2019 GCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAG 2078

Qy       2035 TACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAG 2094
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Qy       2095 CTGGAGAAGCAGCTGGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGAC 2154
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Db       2139 CTGGAGAAGCAGCTGGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGAC 2198

Qy       2155 AGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAG 2214
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Db       2199 AGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAG 2258

Qy       2215 CTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTAC 2274
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Qy       2275 TTGCACTGCACCTTCACCCTGGAGCGTGTCAGCCCCAGCACTAGTGACCTGGCCTGCAAG 2334
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Db       2319 TTGCACTGCACCTTCACCCTGGAGCGTGTCAGCCCCAGCACTAGTGACCTGGCCTGCAAG 2378

Qy       2335 CTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACC 2394
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Qy       2395 AAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTG 2454
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Qy       2515 GACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAACTCCACCTGGAC 2574
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Qy       2575 AGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGG 2634
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db       2619 AGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGCGG 2678

Qy       2635 GAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTG 2694
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RESULT 7
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ID   ADH71635 standard; DNA; 2881 BP.
XX
AC   ADH71635;
XX
DT   25-MAR-2004  (first entry)
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DE   Human gene of the invention NOV21n SEQ ID NO:531.
XX
KW   ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW   anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW   vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW   obesity; diabetes; infectious disease; metabolic syndrome X;
KW   dyslipidaemia.
XX
OS   Homo sapiens.
XX
PN   WO2003102155-A2.
XX
PD   11-DEC-2003.
XX
PF   03-JUN-2003; 2003WO-US017430.
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XX

PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386864P.
PR 06-JUN-2002; 2002US-0387016P.
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PR 07-JUN-2002; 2002US-0386816P.
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PR 08-JUN-2002; 2002US-0296960P.
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PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
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PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
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PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
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PR 13-AUG-2002; 2002US-0403459P.
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PR 27-AUG-2002; 2002US-0406240P.
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PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
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PR 09-OCT-2002; 2002US-0417406P.
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PR 28-OCT-2002; 2002US-0421156P.
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PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX
DR WPI; 2004-081935/08.
DR P-PSDB; ADH71636.
XX
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
PS Example 21; SEQ ID NO 531; 1880pp; English.
XX
CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.

XX
SQ Sequence 2881 BP; 527 A; 985 C; 867 G; 502 T; 0 U; 0 Other;

Query Match 97.2%; Score 2674.8; DB 12; Length 2881;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2727; Conservative 0; Mismatches 22; Indels 9; Gaps 3;

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Qy          1 CCGCGGGGCCCCGCGCCCGGCCCGCCCGCCTGCCCGCCCGCGGCCATGGCCGTCCGGCCC 60
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Db         42 CCGCGGGGCCCCGCGCCCGGCCCGCCCGCCTGCCCGCCCGCGGCCATGGCCGTCCGGCCC 101

Qy         61 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 161

Qy        121 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC 221

Qy        181 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        301 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGC 360
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Qy        421 TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 480
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Db        462 TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 521

Qy        481 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 540
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Qy        541 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        762 ATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGG 821

Qy        781 TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG 840
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Qy        901 GTCCAGAA---AACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGG 957
              |||||  |    || | || | |    ||   | | || ||||||||||||||||||||
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1002 AGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGAC 1061

Qy       1018 CCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGT 1077
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1062 CCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGT 1121

Qy       1078 ACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGC 1137
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Db       1122 ACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGC 1181

Qy       1138 CTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCTCATCCTCGTTTATTGC 1197
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Db       1182 CTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCTCATCCTCGTTTATTGC 1241

Qy       1198 CGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTC 1257
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Db       1242 CGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTC 1301

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Db       1302 CAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCG 1361

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Qy       1558 TTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCCAGAT 1617
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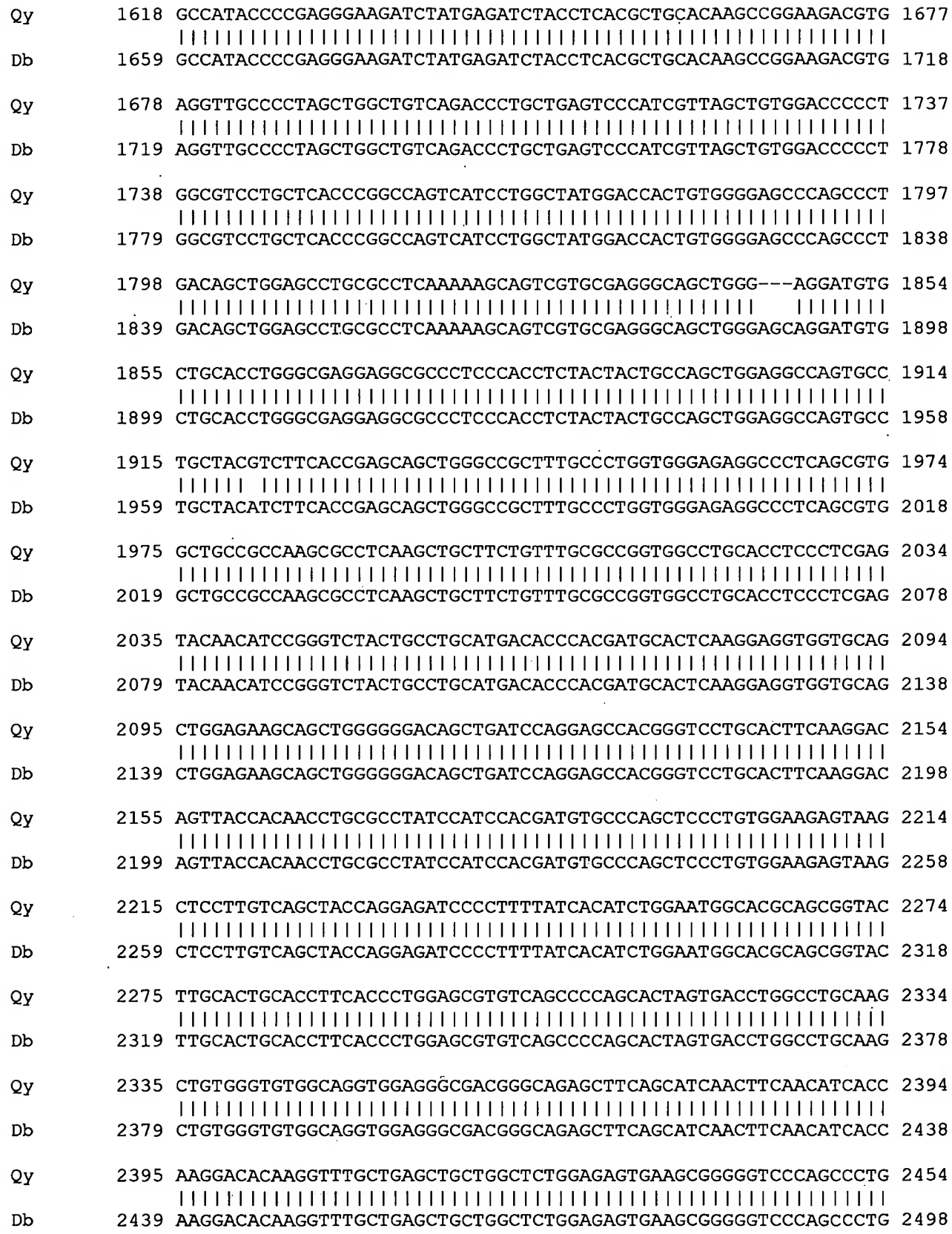
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Qy 1915 TGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTG 1974
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Qy 2035 TACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAG 2094
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RESULT 8
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ID ADH71637 standard; DNA; 2881 BP.
XX
AC ADH71637;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human gene of the invention NOV21o SEQ ID NO:533.
XX
KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
PF 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
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XX
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PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
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PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
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PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX
DR WPI; 2004-081935/08.
DR P-PSDB; ADH71638.
XX
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
PS Example 21; SEQ ID NO 533; 1880pp; English.
XX
CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 2881 BP; 527 A; 985 C; 867 G; 502 T; 0 U; 0 Other;

Query Match 97.2%; Score 2674.8; DB 12; Length 2881;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2727; Conservative 0; Mismatches 22; Indels 9; Gaps 3;

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Db 42 CCGCGGGGCCCCGCGCCCGGCCCGCCCGCCTGCCCGCCCGCGGCCATGGCCGTCCGGCCC 101

Qy 61 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 120
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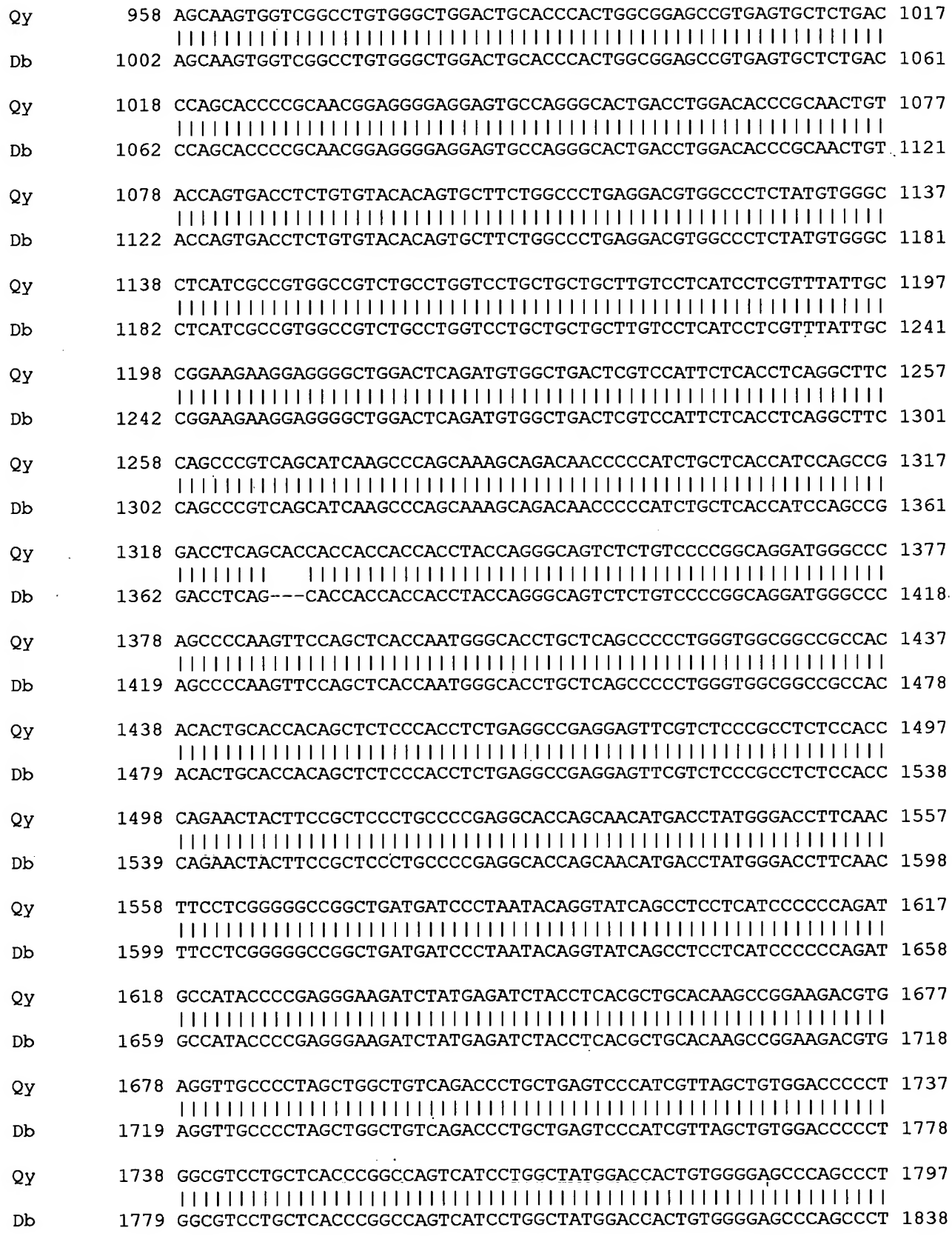
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Db       2319 TTGCACTGCACCTTCACCCTGGAGCGTGTCAGCCCCAGCACTAGTGACCTGGCCTGCAAG 2378

Qy       2335 CTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACC 2394
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Db       2379 CTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACC 2438

Qy       2395 AAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTG 2454
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Db       2439 AAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTG 2498

Qy       2455 GTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTG 2514
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Qy       2515 GACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAACTCCACCTGGAC 2574
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Db       2559 GACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAACTCCACCTGGAC 2618

Qy       2575 AGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGG 2634
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Db       2619 AGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGG 2678

Qy       2635 GAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTG 2694
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Qy       2695 GGCCAGCCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGAGGCCGGCCAG 2752
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RESULT 9
ADH71641
ID   ADH71641 standard; DNA; 2881 BP.
XX
AC   ADH71641;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Human gene of the invention NOV21q SEQ ID NO:537.
XX
KW   ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW   anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW   vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW   obesity; diabetes; infectious disease; metabolic syndrome X;
KW   dyslipidaemia.
XX
OS   Homo sapiens.
XX
PN   WO2003102155-A2.
XX
PD   11-DEC-2003.
XX
PF   03-JUN-2003; 2003WO-US017430.
XX
PR   03-JUN-2002; 2002US-0385120P.
PR   04-JUN-2002; 2002US-0385784P.
PR   05-JUN-2002; 2002US-0386041P.
PR   05-JUN-2002; 2002US-0386047P.
PR   06-JUN-2002; 2002US-0386376P.
PR   06-JUN-2002; 2002US-0386453P.
PR   06-JUN-2002; 2002US-0386864P.
PR   06-JUN-2002; 2002US-0387016P.
PR   07-JUN-2002; 2002US-0386796P.
PR   07-JUN-2002; 2002US-0386816P.
PR   07-JUN-2002; 2002US-0386931P.
PR   07-JUN-2002; 2002US-0386942P.
PR   07-JUN-2002; 2002US-0386971P.
PR   07-JUN-2002; 2002US-0387262P.
PR   08-JUN-2002; 2002US-0296960P.
PR   10-JUN-2002; 2002US-0387400P.
PR   10-JUN-2002; 2002US-0387535P.
PR   11-JUN-2002; 2002US-0387610P.
PR   11-JUN-2002; 2002US-0387625P.
PR   11-JUN-2002; 2002US-0387634P.
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PR   11-JUN-2002; 2002US-0387696P.
PR   11-JUN-2002; 2002US-0387702P.
PR   11-JUN-2002; 2002US-0387836P.
PR   11-JUN-2002; 2002US-0387859P.
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PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389144P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389729P.
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PR 19-JUN-2002; 2002US-0390006P.
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PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402156P.
PR 09-AUG-2002; 2002US-0402256P.
PR 09-AUG-2002; 2002US-0402389P.
PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
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PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
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PR 23-SEP-2002; 2002US-0412731P.
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PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
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PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;

PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX
DR WPI; 2004-081935/08.
DR P-PSDB; ADH71642.
XX
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
PS Example 21; SEQ ID NO 537; 1880pp; English.
XX
CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 2881 BP; 526 A; 986 C; 867 G; 502 T; 0 U; 0 Other;

Query Match 97.2%; Score 2674.8; DB 12; Length 2881;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2727; Conservative 0; Mismatches 22; Indels 9; Gaps 3;

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Qy          1 CCGCGGGGCCCCGCGCCCGGCCCGCCCGCCTGCCCGCCCGCGGCCATGGCCGTCCGGCCC 60
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Db         42 CCGCGGGGCCCCGCGCCCGGCCCGCCCGCCTGCCCGCCCGCGGCCATGGCCGTCCGGCCC 101

Qy         61 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 120
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Qy        121 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC 180
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Db        162 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC 221

Qy        181 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 240
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Qy        241 AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 300
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Qy        301 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGC 360
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Db        342 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGTGAGCCGACCATGGAGGTCCGC 401

Qy        361 ATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCGGGCTGGAGGAATACTGGTGCCAG 420
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Db        402 ATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCGGGCTGGAGGAATACTGGTGCCAG 461

Qy        421 TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 480
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Db        462 TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 521

Qy        481 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 540
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Db        522 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 581

Qy        541 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600
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Db        582 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 641

Qy        601 AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        642 AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 701

Qy        661 CTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAAC 720
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Db        702 CTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAAC 761

Qy        721 ATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGG 780
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Qy        781 TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG 840
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Qy        841 AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT 900
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Db        882 AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT 941

Qy        901 GTCCAGAA---AACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGG 957
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Db        942 GTCCATGACCGCACCGTCTCCTCTCTGCTTGTCTCTGTGGACGGCAGCTGGAGCCCGTGG 1001

Qy        958 AGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGAC 1017
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Db       1002 AGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGAC 1061

Qy       1018 CCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGT 1077
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Qy       1078 ACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGC 1137
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Db       1122 ACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGC 1181
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Qy       1138 CTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCTCATCCTCGTTTATTGC 1197
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Db       1182 CTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCTCATCCTCGTTTATTGC 1241

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Db       1242 CGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTC 1301

Qy       1258 CAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCG 1317
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Db       1302 CAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCG 1361

Qy       1318 GACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCC 1377
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Db       1362 GACCTCAG---CACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCC 1418

Qy       1378 AGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCAC 1437
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Db       1419 AGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCAC 1478

Qy       1438 ACACTGCACCACAGCTCTCCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACC 1497
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Qy       1498 CAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAAC 1557
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Db       1539 CAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAAC 1598

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Qy       1678 AGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCCT 1737
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Qy       1855 CTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCC 1914
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Qy       1915 TGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTG 1974
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Qy       1975 GCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAG 2034
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Qy        2215 CTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTAC 2274
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Db        2259 CTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTAC 2318

Qy        2275 TTGCACTGCACCTTCACCCTGGAGCGTGTCAGCCCCAGCACTAGTGACCTGGCCTGCAAG 2334
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Qy        2335 CTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACC 2394
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Db        2379 CTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACC 2438

Qy        2395 AAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTG 2454
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2439 AAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTG 2498

Qy        2455 GTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTG 2514
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Db        2499 GTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTG 2558

Qy        2515 GACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAACTCCACCTGGAC 2574
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Db        2559 GACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAACTCCACCTGGAC 2618

Qy        2575 AGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGG 2634
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Db        2619 AGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGG 2678

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Db        2739 GGCCAGCCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGAGGCCGGCCAG 2796


RESULT 10
ADH71629
ID   ADH71629 standard; DNA; 2881 BP.
XX
AC   ADH71629;
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XX

DT 25-MAR-2004 (first entry)

XX

DE Human gene of the invention NOV21k SEQ ID NO:525.

XX

KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.

XX

OS Homo sapiens.

XX

PN WO2003102155-A2.

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PD 11-DEC-2003.

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PF 03-JUN-2003; 2003WO-US017430.

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PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
PR 06-JUN-2002; 2002US-0386453P.
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PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390209P.
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PR 17-JUL-2002; 2002US-0396706P.
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PA (CURA-) CURAGEN CORP.
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PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
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DR WPI; 2004-081935/08.
DR P-PSDB; ADH71630.
XX
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.

XX
PS Example 21; SEQ ID NO 525; 1880pp; English.
XX
CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
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SQ Sequence 2881 BP; 526 A; 986 C; 868 G; 501 T; 0 U; 0 Other;

Query Match 97.2%; Score 2674.8; DB 12; Length 2881;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2727; Conservative 0; Mismatches 22; Indels 9; Gaps 3;

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Db        402 ATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCGGGCTGGAGGAATACTGGTGCCAG 461

Qy        421 TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 480
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Db        462 TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 521
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Qy        481 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 540
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Qy        541 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600
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Qy        601 AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 660
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Qy        661 CTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAAC 720
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Qy        721 ATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGG 780
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Qy        781 TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG 840
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Db        822 TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG 881

Qy        841 AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT 900
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Db       1122 ACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGC 1181

Qy       1138 CTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCTCATCCTCGTTTATTGC 1197
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Qy       1198 CGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTC 1257
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Qy       1258 CAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCG 1317
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Qy       1318 GACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCC 1377
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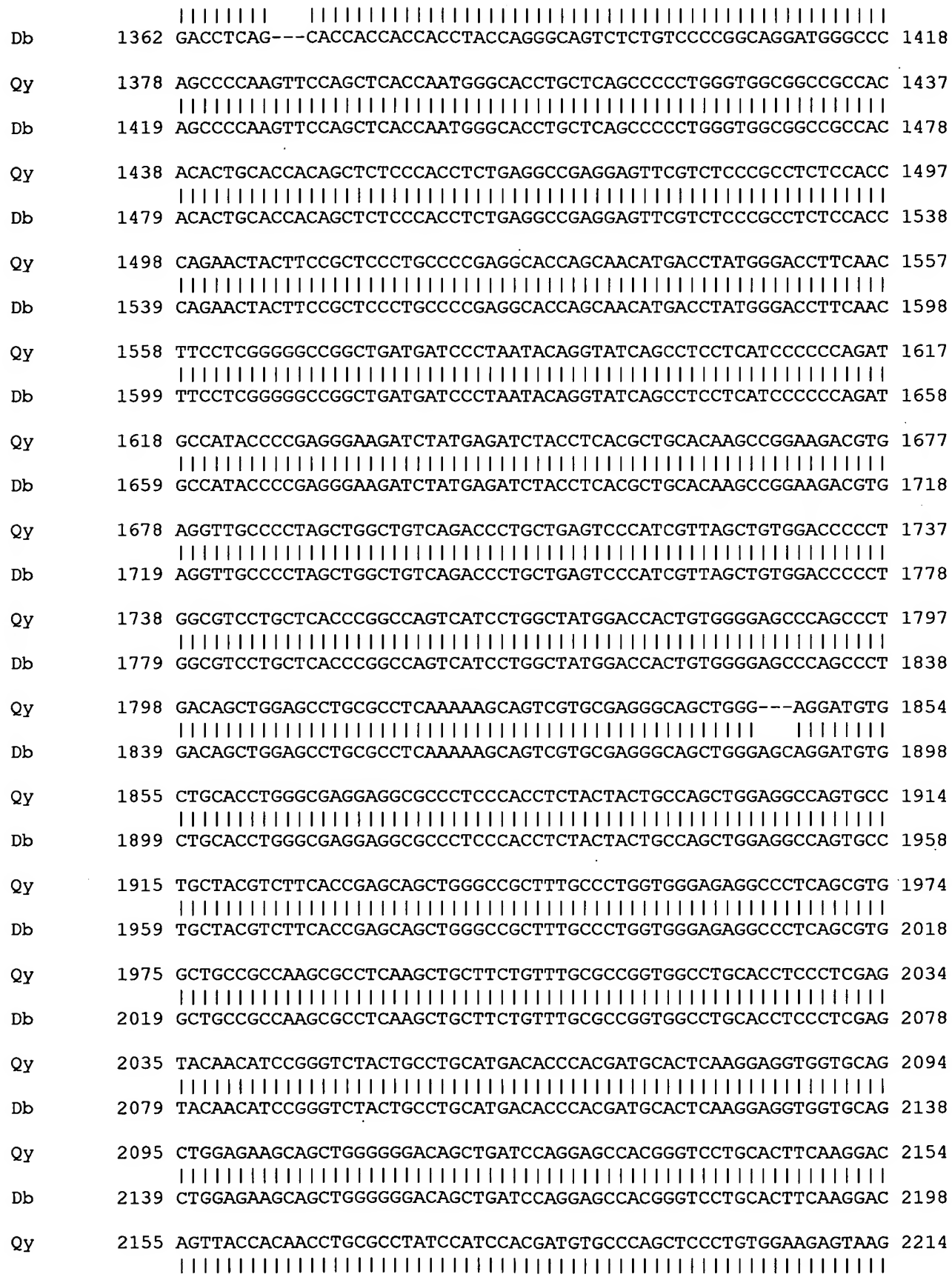

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ID   ADH71631 standard; DNA; 2881 BP.
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AC   ADH71631;
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DT   25-MAR-2004  (first entry)
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XX
KW   ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW   anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW   vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW   obesity; diabetes; infectious disease; metabolic syndrome X;
KW   dyslipidaemia.
XX
OS   Homo sapiens.
XX
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PN WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
PF 03-JUN-2003; 2003WO-US017430.
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PR 03-JUN-2002; 2002US-0385120P.
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PR 05-NOV-2002; 2002US-00423798.
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DR WPI; 2004-081935/08.
DR P-PSDB; ADH71632.
XX
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
PS Example 21; SEQ ID NO 527; 1880pp; English.
XX
CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,

CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 2881 BP; 526 A; 984 C; 868 G; 503 T; 0 U; 0 Other;

Query Match 97.2%; Score 2674.8; DB 12; Length 2881;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2727; Conservative 0; Mismatches 22; Indels 9; Gaps 3;

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Db         42 CCGCGGGGCCCCGCGCCCGGCCCGCCCGCCTGCCCGCCCGCGGCCATGGCCGTCCGGCCC 101

Qy         61 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 120
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Db        162 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC 221

Qy        181 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 240
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Db        222 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 281

Qy        241 AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 300
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Qy        301 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGC 360
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Qy        481 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 540
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Db        522 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 581

Qy        541 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600
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Qy        601 AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 660
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Db        762 ATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGG 821

Qy        781 TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG 840

Db        822 TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG 881

Qy        841 AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT 900

Db        882 AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT 941

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Db       1002 AGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGAC 1061

Qy       1018 CCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGT 1077

Db       1062 CCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGT 1121

Qy       1078 ACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGC 1137

Db       1122 ACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGC 1181

Qy       1138 CTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCTCATCCTCGTTTATTGC 1197

Db       1182 CTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCTCATCCTCGTTTATTGC 1241

Qy       1198 CGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTC 1257

Db       1242 CGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTC 1301

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Db       1362 GACCTCAG---CACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCC 1418

Qy       1378 AGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCAC 1437

Db       1419 AGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCAC 1478

Qy       1438 ACACTGCACCACAGCTCTCCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACC 1497

Db       1479 ACACTGCACCACAGCTCTCCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACC 1538

Qy       1498 CAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAAC 1557
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Qy       1738 GGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCT 1797
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Db       2379 CTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACC 2438
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Qy       2395 AAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTG 2454
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RESULT 12
ADH71645
ID ADH71645 standard; DNA; 2881 BP.
XX
AC ADH71645;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human gene of the invention NOV21s SEQ ID NO:541.
XX
KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
PF 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
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PR 06-JUN-2002; 2002US-0387016P.
PR 07-JUN-2002; 2002US-0386796P.
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PR 20-SEP-2002; 2002US-0412528P.
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PR 09-OCT-2002; 2002US-0417186P.
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PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
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XX
PA (CURA-) CURAGEN CORP.
XX
PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX
DR WPI; 2004-081935/08.
DR P-PSDB; ADH71646.
XX
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
PS Example 21; SEQ ID NO 541; 1880pp; English.
XX
CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 2881 BP; 526 A; 986 C; 868 G; 501 T; 0 U; 0 Other;

Query Match 97.2%; Score 2674.8; DB 12; Length 2881;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2727; Conservative 0; Mismatches 22; Indels 9; Gaps 3;

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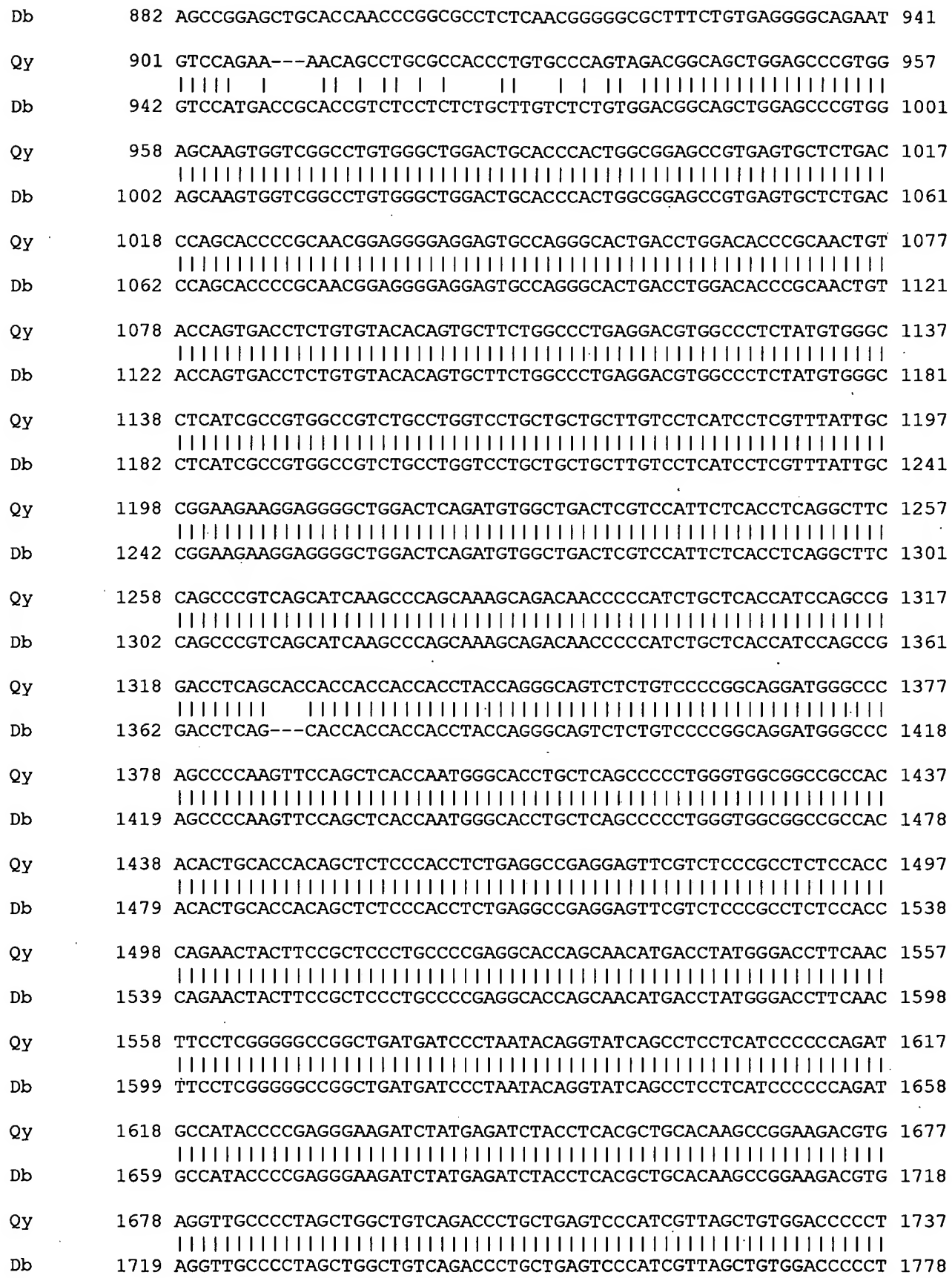

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Qy       1798 GACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGG---AGGATGTG 1854
             ||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||||
Db       1839 GACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGCAGGATGTG 1898

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Db       1899 CTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCC 1958

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Db       2619 AGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGG 2678

Qy       2635 GAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTG 2694
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Qy       2695 GGCCAGCCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGAGGCCGGCCAG 2752
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Db       2739 GGCCAGCCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGAGGCCGGCCAG 2796
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RESULT 13
ADH71627
ID ADH71627 standard; DNA; 2881 BP.
XX
AC ADH71627;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human gene of the invention NOV21j SEQ ID NO:523.
XX
KW ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
PF 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
PR 06-JUN-2002; 2002US-0386376P.
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PR 10-JUN-2002; 2002US-0387400P.
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PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387625P.
PR 11-JUN-2002; 2002US-0387634P.

PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387702P.
PR 11-JUN-2002; 2002US-0387836P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387933P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389118P.
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PR 14-JUN-2002; 2002US-0389144P.
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PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
PR 06-AUG-2002; 2002US-0401628P.
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PR 12-AUG-2002; 2002US-0402786P.
PR 12-AUG-2002; 2002US-0402816P.
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PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
PR 09-OCT-2002; 2002US-0417186P.
PR 09-OCT-2002; 2002US-0417406P.
PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX

PA (CURA-) CURAGEN CORP.
XX
PI Alsobrook JP, Alvarez E, Anderson DW, Boldog FL, Casman SJ;
PI Catterton E, Chapoval A, Crabtree-Bokor JR, Edinger SR, Ellerman K;
PI Ettenberg S, Gangolli EA, Gerlach VL, Gorman L, Gunther E, Guo X;
PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX
DR WPI; 2004-081935/08.
DR P-PSDB; ADH71628.
XX
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
PS Example 21; SEQ ID NO 523; 1880pp; English.
XX
CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 2881 BP; 525 A; 985 C; 869 G; 502 T; 0 U; 0 Other;

Query Match 97.2%; Score 2674.8; DB 12; Length 2881;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2727; Conservative 0; Mismatches 22; Indels 9; Gaps 3;

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Qy          1 CCGCGGGGCCCCGCGCCCGGCCCGCCCGCCTGCCCGCCCGCGGCCATGGCCGTCCGGCCC 60
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Db         42 CCGCGGGGCCCCGCGCCCGGCCCGCCCGCCTGCCCGCCCGCGGCCATGGCCGTCCGGCCC 101

Qy         61 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 161

Qy        121 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC 221

Qy        181 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 240
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Db        222 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 281

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Db        282 AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 341

Qy        301 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGC 360
              |||||||||||||||||||||||||||||||||||    ||| ||||||||||||||||
Db        342 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGTGAGCCGACCATGGAGGTCCGC 401

Qy        361 ATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCGGGCTGGAGGAATACTGGTGCCAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        402 ATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCGGGCTGGAGGAATACTGGTGCCAG 461

Qy        421 TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 480
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Qy        481 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 540
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Qy        541 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        582 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 641

Qy        601 AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        642 AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 701

Qy        661 CTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAAC 720
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Db        762 ATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGG 821

Qy        781 TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        841 AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        882 AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT 941

Qy        901 GTCCAGAA---AACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGG 957
              |||||  |    || | || | |    ||   | | || ||||||||||||||||||||
Db        942 GTCCATGACCGCACCGTCTCCTCTCTGCTTGTCTCTGTGGACGGCAGCTGGAGCCCGTGG 1001

Qy        958 AGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGAC 1017
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1078 ACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGC 1137
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Qy       1138 CTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCTCATCCTCGTTTATTGC 1197
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Qy       1378 AGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCAC 1437
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Db       1419 AGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCAC 1478

Qy       1438 ACACTGCACCACAGCTCTCCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACC 1497
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Db       1479 ACACTGCACCACAGCTCTCCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACC 1538

Qy       1498 CAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAAC 1557
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Qy       1855 CTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCC 1914
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Qy       1915 TGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTG 1974
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Qy       1975 GCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAG 2034
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Qy       2155 AGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAG 2214
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Db       2379 CTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACC 2438

Qy       2395 AAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGGTCCCAGCCCTG 2454
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2455 GTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTG 2514
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Qy       2575 AGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGG 2634
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Qy       2635 GAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTG 2694
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Qy       2695 GGCCAGCCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGAGGCCGGCCAG 2752
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Db       2739 GGCCAGCCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGAGGCCGGCCAG 2796
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RESULT 14
ADH71639
ID   ADH71639 standard; DNA; 2881 BP.
XX
AC   ADH71639;
XX
DT   25-MAR-2004 (first entry)
XX
DE   Human gene of the invention NOV21p SEQ ID NO:535.
XX
KW   ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW   anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW   vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
KW   obesity; diabetes; infectious disease; metabolic syndrome X;
KW   dyslipidaemia.
XX
OS   Homo sapiens.
XX
PN   WO2003102155-A2.
XX
PD   11-DEC-2003.
XX
PF   03-JUN-2003; 2003WO-US017430.
XX
PR   03-JUN-2002; 2002US-0385120P.
PR   04-JUN-2002; 2002US-0385784P.
PR   05-JUN-2002; 2002US-0386041P.
PR   05-JUN-2002; 2002US-0386047P.
PR   06-JUN-2002; 2002US-0386376P.
PR   06-JUN-2002; 2002US-0386453P.
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PR   12-JUN-2002; 2002US-0388096P.
PR   13-JUN-2002; 2002US-0389123P.
PR   14-JUN-2002; 2002US-0389118P.
PR   14-JUN-2002; 2002US-0389120P.

PR 14-JUN-2002; 2002US-0389144P.
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PR 17-JUN-2002; 2002US-0389742P.
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PR 21-JUN-2002; 2002US-0390763P.
PR 17-JUL-2002; 2002US-0396706P.
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PR 13-AUG-2002; 2002US-0403531P.
PR 13-AUG-2002; 2002US-0403532P.
PR 13-AUG-2002; 2002US-0403563P.
PR 13-AUG-2002; 2002US-0406317P.
PR 15-AUG-2002; 2002US-0403617P.
PR 26-AUG-2002; 2002US-0406182P.
PR 26-AUG-2002; 2002US-0406355P.
PR 27-AUG-2002; 2002US-0406240P.
PR 12-SEP-2002; 2002US-0410084P.
PR 20-SEP-2002; 2002US-0412528P.
PR 23-SEP-2002; 2002US-0412731P.
PR 30-SEP-2002; 2002US-0414801P.
PR 30-SEP-2002; 2002US-0414839P.
PR 30-SEP-2002; 2002US-0414840P.
PR 30-SEP-2002; 2002US-0414954P.
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PR 31-OCT-2002; 2002US-0422690P.
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PR 05-NOV-2002; 2002US-00423798.
PR 05-NOV-2002; 2002US-0423798P.
PR 12-NOV-2002; 2002US-0425453P.
XX
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XX
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PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX
DR WPI; 2004-081935/08.

DR P-PSDB; ADH71640.
XX
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
PS Example 21; SEQ ID NO 535; 1880pp; English.
XX
CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising
CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 2881 BP; 525 A; 985 C; 869 G; 502 T; 0 U; 0 Other;

Query Match 97.2%; Score 2674.8; DB 12; Length 2881;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2727; Conservative 0; Mismatches 22; Indels 9; Gaps 3;

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Qy          1 CCGCGGGGCCCCGCGCCCGGCCCGCCCGCCTGCCCGCCCGCGGCCATGGCCGTCCGGCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         42 CCGCGGGGCCCCGCGCCCGGCCCGCCCGCCTGCCCGCCCGCGGCCATGGCCGTCCGGCCC 101

Qy         61 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 GGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCTCCGCGGCTCGGGTGCC 161

Qy        121 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 CAGCAGAGTGCCACCGTGGCCAACCCAGTGCCTGGTGCCAACCCGGACCTGCTTCCCCAC 221

Qy        181 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 TTCCTGGTGGAGCCCGAGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGC 281

Qy        241 AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 AAGGCCGTGCCCGCCACGCAGATCTTCTTCAAGTGCAACGGGGAGTGGGTGCGCCAGGTG 341

Qy        301 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCCACCATGGAGGTCCGC 360
              |||||||||||||||||||||||||||||||||||   ||| ||||||||||||||||
Db        342 GACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGTGAGCCGACCATGGAGGTCCGC 401

Qy        361 ATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCGGGCTGGAGGAATACTGGTGCCAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        402 ATTAATGTCTCAAGGCAGCAGGTCGAGAAGGTGTTCGGGCTGGAGGAATACTGGTGCCAG 461
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Qy        421 TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        462 TGCGTGGCATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCTACATCCGCATAGCC 521

Qy        481 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        522 AGATTGCGCAAGAACTTCGAGCAGGAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGC 581

Qy        541 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        582 ATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGCCGAGGTGGAGTGGCTCCGG 641

Qy        601 AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        642 AACGAGGACCTGGTGGACCCGTCCCTGGACCCCAATGTATACATCACGCGGGAGCACAGC 701

Qy        661 CTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        702 CTGGTGGTGCGACAGGCCCGCCTTGCTGACACGGCCAACTACACCTGCGTGGCCAAGAAC 761

Qy        721 ATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        762 ATCGTGGCACGTCGCCGCAGCGCCTCCGCTGCTGTCATCGTCTACGTGAACGGTGGGTGG 821

Qy        781 TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        822 TCGACGTGGACCGAGTGGTCCGTCTGCAGCGCCAGCTGTGGGCGCGGCTGGCAGAAACGG 881

Qy        841 AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        882 AGCCGGAGCTGCACCAACCCGGCGCCTCTCAACGGGGGCGCTTTCTGTGAGGGGCAGAAT 941

Qy        901 GTCCAGAA---AACAGCCTGCGCCACCCTGTGCCCAGTAGACGGCAGCTGGAGCCCGTGG 957
              |||||  |    || | || | |    ||   | | || ||||||||||||||||||||
Db        942 GTCCATGACCGCACCGTCTCCTCTCTGCTTGTCTCTGTGGACGGCAGCTGGAGCCCGTGG 1001

Qy        958 AGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGAC 1017
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1002 AGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGTGAGTGCTCTGAC 1061

Qy       1018 CCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGT 1077
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1062 CCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGACACCCGCAACTGT 1121

Qy       1078 ACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGC 1137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1122 ACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTGGGC 1181

Qy       1138 CTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCTCATCCTCGTTTATTGC 1197
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Db       1182 CTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCTCATCCTCGTTTATTGC 1241

Qy       1198 CGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTC 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1242 CGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTC 1301
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Qy       1258 CAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCG 1317
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1302 CAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTCACCATCCAGCCG 1361

Qy       1318 GACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCC 1377
             ||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1362 GACCTCAG---CACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGGCAGGATGGGCCC 1418

Qy       1378 AGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCAC 1437
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 AGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGTGGCGGCCGCCAC 1478

Qy       1438 ACACTGCACCACAGCTCTCCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACC 1497
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 ACACTGCACCACAGCTCTCCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACC 1538

Qy       1498 CAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAAC 1557
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 CAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTATGGGACCTTCAAC 1598

Qy       1558 TTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCCAGAT 1617
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Db       1599 TTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTCATCCCCCCAGAT 1658

Qy       1618 GCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGACGTG 1677
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Qy       1738 GGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCT 1797
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Db       1779 GGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGGGAGCCCAGCCCT 1838

Qy       1798 GACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGG---AGGATGTG 1854
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Db       1839 GACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGGGAGCAGGATGTG 1898

Qy       1855 CTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCC 1914
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1899 CTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAGGCCAGTGCC 1958

Qy       1915 TGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTG 1974
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1959 TGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTG 2018

Qy       1975 GCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAG 2034
             |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       2019 GCTGCCGCCAAGCGCCTCAGGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAG 2078

Qy       2035 TACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAG 2094
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Db       2079 TACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAGGTGGTGCAG 2138

Qy       2095 CTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGAC 2154
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Db        2139 CTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCACTTCAAGGAC 2198

Qy        2155 AGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAG 2214
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Db        2199 AGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGGAAGAGTAAG 2258

Qy        2215 CTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTAC 2274
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Db        2259 CTCCTTGTCAGCTACCAGGAGATCCCCTTTTATCACATCTGGAATGGCACGCAGCGGTAC 2318

Qy        2275 TTGCACTGCACCTTCACCCTGGAGCGTGTCAGCCCCAGCACTAGTGACCTGGCCTGCAAG 2334
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Db        2319 TTGCACTGCACCTTCACCCTGGAGCGTGTCAGCCCCAGCACTAGTGACCTGGCCTGCAAG 2378

Qy        2335 CTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACC 2394
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2379 CTGTGGGTGTGGCAGGTGGAGGGCGACGGGCAGAGCTTCAGCATCAACTTCAACATCACC 2438

Qy        2395 AAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTG 2454
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2439 AAGGACACAAGGTTTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGGGTCCCAGCCCTG 2498

Qy        2455 GTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTG 2514
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2499 GTGGGCCCCAGTGCCTTCAAGATCCCCTTCCTCATTCGGCAGAAGATAATTTCCAGCCTG 2558

Qy        2515 GACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAACTCCACCTGGAC 2574
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2559 GACCCACCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAAACTCCACCTGGAC 2618

Qy        2575 AGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGG 2634
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2619 AGCCATCTCAGCTTCTTTGCCTCCAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGG 2678

Qy        2635 GAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTG 2694
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2679 GAGGCGCGGCACTTCCCCAACGGCAACCTCAGCCAGCTGGCTGCAGCAGTGGCTGGACTG 2738

Qy        2695 GGCCAGCCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGAGGCCGGCCAG 2752
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2739 GGCCAGCCAGACGCTGGCCTCTTCACAGTGTCGGAGGCTGAGTGCTGAGGCCGGCCAG 2796


RESULT 15
ADH71643
ID   ADH71643 standard; DNA; 2881 BP.
XX
AC   ADH71643;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Human gene of the invention NOV21r SEQ ID NO:539.
XX
KW   ds; gene; human; cytostatic; immunomodulator; neuroprotective; nootropic;
KW   anorectic; antidiabetic; antimicrobial; antilipaemic; gene therapy;
KW   vaccine; cancer; cachexia; Alzheimer's disease; Parkinson's disease;
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KW obesity; diabetes; infectious disease; metabolic syndrome X;
KW dyslipidaemia.
XX
OS Homo sapiens.
XX
PN WO2003102155-A2.
XX
PD 11-DEC-2003.
XX
PF 03-JUN-2003; 2003WO-US017430.
XX
PR 03-JUN-2002; 2002US-0385120P.
PR 04-JUN-2002; 2002US-0385784P.
PR 05-JUN-2002; 2002US-0386041P.
PR 05-JUN-2002; 2002US-0386047P.
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PR 06-JUN-2002; 2002US-0386453P.
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PR 19-JUN-2002; 2002US-0390209P.
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PR 09-AUG-2002; 2002US-0402389P.

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PR 12-AUG-2002; 2002US-0402816P.
PR 12-AUG-2002; 2002US-0402821P.
PR 12-AUG-2002; 2002US-0402832P.
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PR 13-AUG-2002; 2002US-0403459P.
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PR 09-OCT-2002; 2002US-0417186P.
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PR 23-OCT-2002; 2002US-0420639P.
PR 28-OCT-2002; 2002US-0421156P.
PR 31-OCT-2002; 2002US-0422690P.
PR 01-NOV-2002; 2002US-0423130P.
PR 05-NOV-2002; 2002US-00423798.
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PI Gusev VY, Herrmann JL, Ji W, Kekuda R, Li L, Liu X, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mezick AJ, Millet I, Mishra VS;
PI Padigaru M, Patturajan M, Pena CEA, Peyman JA, Raha D, Rastelli L;
PI Rieger DK, Rothenberg ME, Sciore P, Shenoy SG, Shimkets RA;
PI Smithson G, Spytek KA, Stone DJ, Vernet CAM, Voss EZ, Zhong M;
PI Zhong H;
XX
DR WPI; 2004-081935/08.
DR P-PSDB; ADH71644.
XX
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, diabetes, infection or
PT obesity, and in chromosome mapping, tissue typing or pharmacogenomics.
XX
PS Example 21; SEQ ID NO 539; 1880pp; English.
XX
CC The invention relates to a novel isolated polypeptide (NOVX). A
CC polypeptide of the invention has cytostatic, immunomodulator,
CC neuroprotective, nootropic, anorectic, antidiabetic, antimicrobial, and
CC antilipaemic activity, and may have a use in gene therapy, and as a
CC vaccine. The polypeptides are encoded by NOVX polynucleotides comprising

CC any of the 303 fully defined nucleotide sequences given in the
CC specification. The polypeptide is useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease. The
CC polypeptide, polynucleotide and antibody are useful in diagnosing,
CC treating or preventing NOVX-associated disorders, e.g. cancer, cachexia,
CC Alzheimer's disease, Parkinson's disease, obesity, diabetes, infectious
CC diseases, metabolic syndrome X or dyslipidaemias. The nucleic acids are
CC further used as hybridisation probes, in chromosome mapping, tissue
CC typing, preventive medicine, and pharmacogenomics. The present sequence
CC encodes a NOVX polypeptide of the invention.
XX
SQ Sequence 2881 BP; 527 A; 985 C; 867 G; 502 T; 0 U; 0 Other;

Query Match 97.2%; Score 2674.8; DB 12; Length 2881;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2727; Conservative 0; Mismatches 22; Indels 9; Gaps 3;

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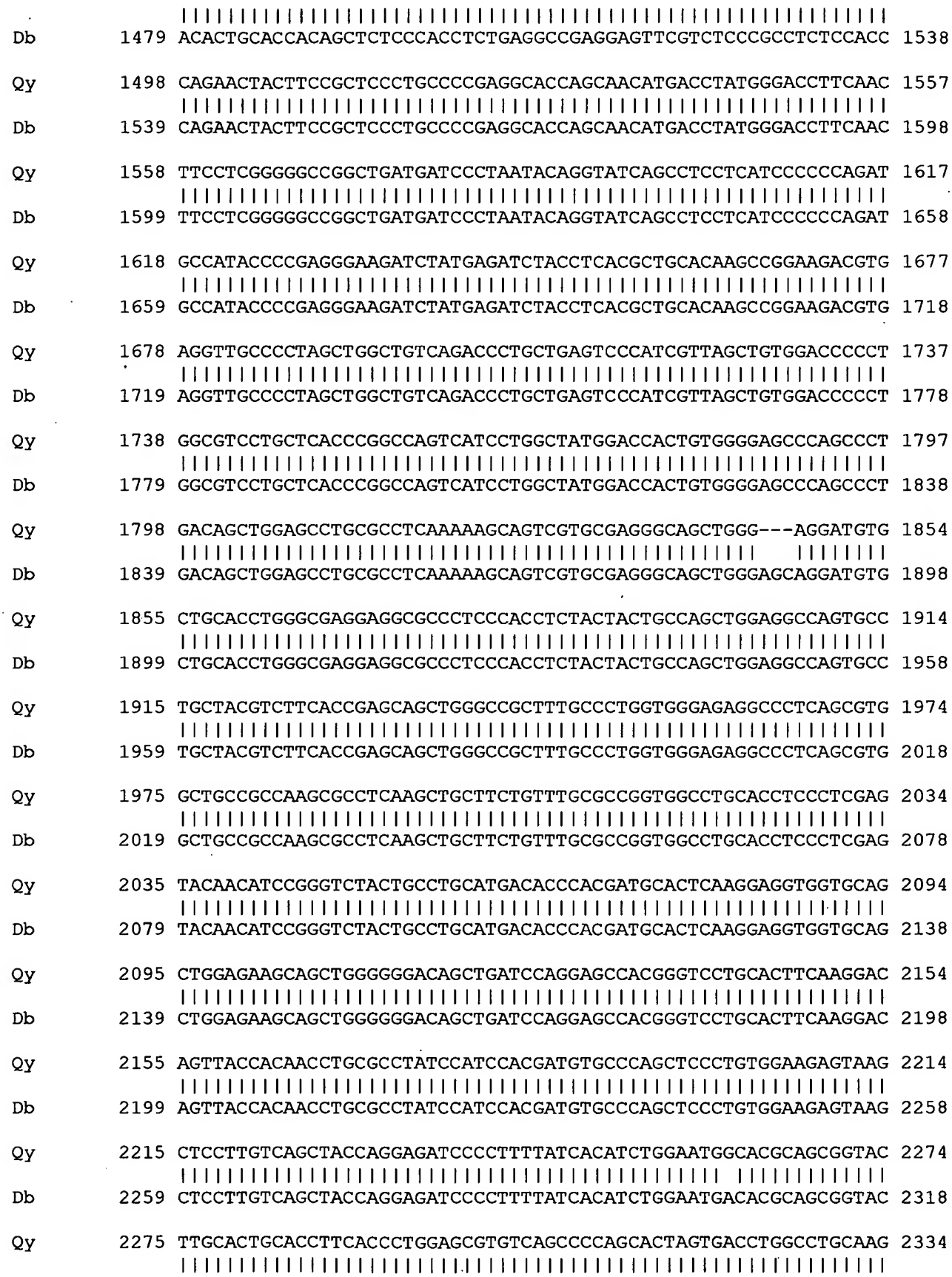

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Search completed: March 5, 2005, 22:58:50
Job time : 1411 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2005, 19:26:23 ; Search time 433.33 Seconds
(without alignments)
10391.692 Million cell updates/sec

Title: US-10-624-932-1
Perfect score: 2752
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2259	82.1	3014	2	US-08-808-982-1	Sequence 1, Appli
2	2259	82.1	3014	3	US-09-306-902A-1	Sequence 1, Appli
3	1562.4	56.8	1787	2	US-08-808-982-2	Sequence 2, Appli
4	1562.4	56.8	1787	3	US-09-306-902A-2	Sequence 2, Appli
5	841.4	30.6	2831	2	US-08-808-982-3	Sequence 3, Appli
6	841.4	30.6	2831	3	US-09-306-902A-3	Sequence 3, Appli
7	833.6	30.3	3008	4	US-09-949-016-4794	Sequence 4794, Ap
8	487	17.7	2736	4	US-09-969-532-9	Sequence 9, Appli
9	487	17.7	3411	4	US-09-969-532-33	Sequence 33, Appl
10	467	17.0	2703	4	US-09-969-532-11	Sequence 11, Appl
11	460.2	16.7	2694	4	US-09-969-532-13	Sequence 13, Appl

	12	439.8	16.0	2661	4	US-09-969-532-15	Sequence 15, Appl
	13	323	11.7	349	4	US-09-471-276-345	Sequence 345, App
	14	293.2	10.7	1968	4	US-09-969-532-31	Sequence 31, Appl
	15	293.2	10.7	2001	4	US-09-969-532-29	Sequence 29, Appl
	16	293.2	10.7	2010	4	US-09-969-532-27	Sequence 27, Appl
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	20	284.8	10.3	1701	4	US-09-969-532-3	Sequence 3, Appli
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ALIGNMENTS

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US-08-808-982-1
; Sequence 1, Application US/08808982
; Patent No. 5939271
;  GENERAL INFORMATION:
;    APPLICANT:  Tessier-Lavigne, Marc
;    APPLICANT:  Leonardo, E. David
;    APPLICANT:  Hink, Lindsay
;    APPLICANT:  Masu, Masayuki
;    APPLICANT:  Kazuko, Keino-Masu
;    TITLE OF INVENTION:  Netrin Receptors
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;      STREET:  268 BUSH STREET, SUITE 3200
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
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;       ZIP:  94104
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/808,982
;       FILING DATE:
;       CLASSIFICATION:  530
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  OSMAN, RICHARD A
;       REGISTRATION NUMBER:  36,627
;       REFERENCE/DOCKET NUMBER:  UC96-217
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 343-4341
;       TELEFAX:  (415) 343-4342
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3014 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-808-982-1

  Query Match             82.1%;  Score 2259;  DB 2;  Length 3014;
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Qy      946 TGGAGCCCGTGGAGCAAGTGGTCGGCCTGTGGGCTGGACTGCACCCACTGGCGGAGCCGT 1005
            |||||  ||||||| |||||||| |||||||||| ||||||||||||||||||||||||
Db      901 TGGAGTTCGTGGAGTAAGTGGTCAGCCTGTGGGCTTGACTGCACCCACTGGCGGAGCCGC 960

Qy     1006 GAGTGCTCTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTGACCTGGAC 1065
            |||||||||||||||||||||||||| ||||| |||||||| | |||  ||||||||||
Db      961 GAGTGCTCTGACCCAGCACCCCGCAATGGAGGTGAGGAGTGTCGGGGTGCTGACCTGGAC 1020

Qy     1066 ACCCGCAACTGTACCAGTGACCTCTGTGTACACAGTGCTTCTGGCCCTGAGGACGTGGCC 1125
            |||||||||||||||||||||||||  | ||||  |||||| |||| ||||||||||
Db     1021 ACCCGCAACTGTACCAGTGACCTCTGCCTGCACACCGCTTCTTGCCCCGAGGACGTGGCT 1080

Qy     1126 CTCTATGTGGGCCTCATCGCCGTGGCCGTCTGCCTGGTCCTGCTGCTGCTTGTCCTCATC 1185
            |||||  | |||||  |||| ||||| || |||||  || ||||| |||| | |||
Db     1081 CTCTACATCGGCCTTGTCGCTGTGGCTGTGTGCCTCTTCTTGCTGTTGCTGGCCCTTGGA 1140

Qy     1186 CTCGTTTATTGCCGGAAGAAGGAGGGGCTGGACTCAGATGTGGCTGACTCGTCCATTCTC 1245
            ||| |||| || || |||||||| |||||||||| |||||||| |||||||||| |||
Db     1141 CTCATTTACTGTCGCAAGAAGGAAGGGCTGGACTCCGATGTGGCCGACTCGTCCATCCTC 1200

Qy     1246 ACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCATCTGCTC 1305
            ||||| |||||||||| |||||||||||||||||||||||||||||||||| ||||||
Db     1201 ACCTCGGGCTTCCAGCCTGTCAGCATCAAGCCCAGCAAAGCAGACAACCCCCACCTGCTC 1260
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Qy       1306 ACCATCCAGCCGGACCTCAGCACCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGG 1365
             |||||||||||| |||||||||||||||| |||||||||||||||||||| ||| |  ||
Db       1261 ACCATCCAGCCAGACCTCAGCACCACCACTACCACCTACCAGGGCAGTCTATGTTCGAGG 1320

Qy       1366 CAGGATGGGCCCAGCCCCAAGTTCCAGCTCACCAATGGGCACCTGCTCAGCCCCCTGGGT 1425
             |||||||| |||||||||||||||||||| | ||||| |||||||||||||| |||||
Db       1321 CAGGATGGACCCAGCCCCAAGTTCCAGCTCTCTAATGGTCACCTGCTCAGCCCACTGGGG 1380

Qy       1426 GGCGGCCGCCACACACTGCACCACAGCTCTCCCACCTCTGAGGCCGAGGAGTTCGTCTCC 1485
              | |||||||| ||  |||||||||||| |||||||||||||| ||||| |||||||||
Db       1381 AGTGGCCGCCATACGTTGCACCACAGCTCACCCACCTCTGAGGCTGAGGACTTCGTCTCC 1440

Qy       1486 CGCCTCTCCACCCAGAACTACTTCCGCTCCCTGCCCCGAGGCACCAGCAACATGACCTAT 1545
             |||||||||||||| |||||||| || |||||||||| |||||||||||||||| ||||
Db       1441 CGCCTCTCCACCCAAAACTACTTTCGTTCCCTGCCCCGCGGCACCAGCAACATGGCCTAC 1500

Qy       1546 GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACAGGTATCAGCCTCCTC 1605
             |||||||||||||||||||||||||||||||||||||||||||||||| || ||||||||||||
Db       1501 GGGACCTTCAACTTCCTCGGGGGCCGGCTGATGATCCCTAATACGGGGATCAGCCTCCTC 1560

Qy       1606 ATCCCCCCAGATGCCATACCCCGAGGGAAGATCTATGAGATCTACCTCACGCTGCACAAG 1665
             || ||||| |||||||| |||||||| |||||||| |||||||||||||| |||||||||
Db       1561 ATACCCCCGGATGCCATCCCCCGAGGAAAGATCTACGAGATCTACCTCACACTGCACAAG 1620

Qy       1666 CCGGAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCCATCGTTAGC 1725
             || ||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||
Db       1621 CCAGAAGACGTGAGGTTGCCCCTAGCTGGCTGTCAGACCCTGCTGAGTCCAGTCGTTAGC 1680

Qy       1726 TGTGGACCCCCTGGCGTCCTGCTCACCCGGCCAGTCATCCTGGCTATGGACCACTGTGGG 1785
             ||||| ||||| || |||||||||||||||||||||||| || ||||||||||||||
Db       1681 TGTGGGCCCCCAGGAGTCCTGCTCACCCGGCCAGTCATCCTTGCAATGGACCACTGTGGA 1740

Qy       1786 GAGCCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAGTCGTGCGAGGGCAGCTGG 1845
             |||||||||||||||||||| |||||||||||||||||| |||||||||| |||
Db       1741 GAGCCCAGCCCTGACAGCTGGAGTCTGCGCCTCAAAAAGCAGTCCTGCGAGGGCAGTTGG 1800

Qy       1846 GAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCCACCTCTACTACTGCCAGCTGGAG 1905
             |||||||||||||||| || |||||| | || |||||||||||||||||||||||||
Db       1801 GAGGATGTGCTGCACCTTGGTGAGGAGTCACCTTCCCACCTCTACTACTGCCAGCTGGAG 1860

Qy       1906 GCCAGTGCCTGCTACGTCTTCACCGAGCAGCTGGGCCGCTTTGCCCTGGTGGGAGAGGCC 1965
             ||| | |||||||| |||||||| |||||||||||||||||||||||| |||||||||
Db       1861 GCCGGGGCCTGCTATGTCTTCACGGAGCAGCTGGGCCGCTTTGCCCTGGTAGGAGAGGCC 1920

Qy       1966 CTCAGCGTGGCTGCCGCCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACC 2025
             ||||||||||||||.|||||||||||| ||| |||||||||| || |||||||| ||
Db       1921 CTCAGCGTGGCTGCCACCAAGCGCCTCAGGCTCCTTCTGTTTGCTCCCGTGGCCTGTACG 1980

Qy       2026 TCCCTCGAGTACAACATCCGGGTCTACTGCCTGCATGACACCCACGATGCACTCAAGGAG 2085
             ||||| |||||||||||||| || |||||||| || |||||||||| || |||||||||
Db       1981 TCCCTTGAGTACAACATCCGAGTGTACTGCCTACACGACACCCACGACGCTCTCAAGGAG 2040

Qy       2086 GTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACGGGTCCTGCAC 2145
             |||||||||||||||||||||| || |||||||||||||||||| || |||||||||
Db       2041 GTGGTGCAGCTGGAGAAGCAGCTAGGTGGACAGCTGATCCAGGAGCCTCGCGTCCTGCAC 2100

Qy       2146 TTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCCAGCTCCCTGTGG 2205
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